

GenCore version 5.1.1.6

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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:14:49 ; Search time 24 Seconds
(without alignments)

21.554 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12

Perfect score: 58

Sequence: 1 AHKSEVAHFK 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	609	1 ALBU_HUMAN	P02768 homo sapien
2	57	98.3	608	1 ALBU_RAT	P02770 rattus norv
3	54	93.1	600	1 ALBU_MACMU	Q28522 macaca mula
4	54	93.1	609	1 ALBU_MERON	Q35090 meriones un
5	53	91.4	607	1 ALBU_BOVIN	P02769 bos taurus
6	52	89.7	608	1 ALBU_RABIT	P49065 oryctolagus
7	49	84.5	608	1 ALBU_MOUSE	P07724 mus musculus
8	48	82.8	607	1 ALBU_HORSE	P35747 equus caball
9	48	82.8	607	1 ALBU_SHEEP	P14639 ovis aries
10	48	82.8	608	1 ALBU_PIG	P49064 felis silve
11	47	81.0	605	1 ALBU_FIG	P08835 sus scrofa
12	45	77.6	615	1 ALBU_CHICK	P19121 gallus gall
13	44	75.9	40	1 ALBU_TRASC	P81188 trachemys s
14	43	74.1	608	1 ALBU_CANFA	P49822 canis fami
15	37	63.8	1002	1 RBMC_MOUSE	Q84x3 mus musculus
16	36	62.1	719	1 FRE4_YEAST	P53746 saccharomyc
17	35	60.3	155	1 RL22_ARCFU	Q28359 archaeoglob
18	35	60.3	194	1 ITPA_HUMAN	Q9b32 homo sapien
19	35	60.3	324	1 CATV_NPVCD	Q41479 choristoneu
20	35	60.3	1308	1 MAK6_MOUSE	Q9jm52 mus musculus
21	35	60.3	1332	1 MAK6_HUMAN	Q8n4c8 homo sapien
22	34	58.6	200	1 HAM1_CAMJ2	Q9pms6 campylobact
23	34	58.6	478	1 Y143_MYCLE	Q32912 mycobacteri
24	34	58.6	488	1 YJCP_ECOLI	P32714 escherichia
25	34	58.6	512	1 SYM_MYCPN	P75091 mycoplasma
26	34	58.6	520	1 CLIA_BOVIN	P00189 bos taurus
27	34	58.6	520	1 CLIA_CAPHI	P79153 capra hircu
28	34	58.6	625	1 PKN1_THETN	Q8i9t6 thermoanaer
29	34	58.6	685	1 PKN2_CLOPE	Q8x1l8 clostridium
30	34	58.6	1121	1 DPOL_ADEGI	Q64751 avian adeno
31	34	58.6	1597	1 RLRL_YEAST	P53552 saccharomyc
32	33	56.9	185	1 VG16_HAEIN	P71387 haemophilus
33	33	56.9	219	1 YQFA_ECOLI	Q46827 escherichia

RESULT 1

ID	ALBU_HUMAN	STANDARD;	PRT;	609 AA.
AC	P02768; Q95574; Q13140; Q9P157; Q9P117; Q9UHS3; Q9UJZ0;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Serum albumin precursor.			
GN	ALB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86196112; PubMed=3009475;			
RA	Minchetti P.P., Ruffner D.E., Kuang W.J., Dennison O.E., Hawkins J.W.,			
RA	Beattie W.G., Dugaiczak A.;			
RT	"Molecular structure of the human albumin gene is revealed by			
RT	nucleotide sequence within qll-22 of chromosome 4.,";			
RL	J. Biol. Chem. 261:6747-6757(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANT LYS-420.			
RX	MEDLINE=82081982; PubMed=6171778;			
RA	Lawn R.M., Adelman J., Bock S.C., Franke A.E., Houck C.M.,			
RA	Najarian R.C., Seeburg P.H., Wion K.L.;			
RT	"The sequence of human serum albumin cDNA and its expression in E.			
RT	coli.,";			
RL	Nucleic Acids Res. 9:6103-6114(1981).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT GLY-121.			
RX	MEDLINE=82105994; PubMed=6275391;			
RA	Dugaiczak A., Law S.W., Dennison O.E.;			
RT	"Nucleotide sequence and the encoded amino acids of human serum			
RT	albumin mRNA.,";			
RL	Proc. Natl. Acad. Sci. U.S.A. 79:71-75(1982).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Yang S., Zhang R.A., Qi Z.W., Yuan Z.Y.;			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A. (PRO0903/PRO1708/PRO2044/PRO2619/PRO2675).			
RC	TISSUE=Fetal liver;			
RA	Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,			
RA	Xu W., Gao F., Liu M., He F., Zhang Y., Ouyang S., Luo L.;			
RT	"Functional prediction of the coding sequences of 121 new genes			
RT	deduced by analysis of cDNA clones from human fetal liver.,";			
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A., AND VARIANT HIROSHIMA-1 LYS-378.			
RA	Huang M.C., Wu H.T.;			
RT	"The cDNA sequences of human serum albumin.,";			
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			

035723 mus musculu
P47150 saccharomyc
Q00214 homo sapien
Q9j115 mus musculu
Q62665 rattus norv
Q08447 mycobacteri
P34116 ricinus com
P34266 caenorhabdi
Q01262 pseudomonas
P37894 caulobacter
Q64566 rattus norv
Q9s1b3 arabidopsis

ALIGNMENTS

RC TISSUE=Liver, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Kirschner D.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 25-609
RX MEDLINE=76187907; PubMed=1225573;
RA Meloun B., Moravsek L., Kostka V.;
RT "Complete amino acid sequence of human serum albumin.";
RL FEBS Lett. 58:134-137(1975).
RN [9]
RP SEQUENCE OF 25-609
RX Brown J.R., Shockley P., Behrens P.Q.;
RL (In) Bing D.H. (eds.);
RL The chemistry and physiology of the human plasma proteins, pp.23-40,
RL Pergamon Press, New York (1979).
RN [10]
RP SEQUENCE OF 1-455 FROM N.A.
RC TISSUE=Liver;
RA Menaya J., Parrilla R., Ayuso M.S.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=86140099; PubMed=2419329;
RA Urano Y., Watanabe K., Sakai M., Tamaoki T.;
RT "The human albumin gene. Characterization of the 5' and 3' flanking
regions and the polymorphic gene transcripts.";
RL J. Biol. Chem. 261:3244-3251(1986).
RN [12]
RP SEQUENCE OF 222-229.
RX MEDLINE=76257808; PubMed=955075;
RA Walker J.E.;
RT "Lysine residue 199 of human serum albumin is modified by
acetylsalicylic acid.";
RL FEBS Lett. 66:173-175(1976).
RN [13]
RP SEQUENCE OF 25-44 AND 480-499.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
1994.";
RL Electrophoresis 15:1459-1465(1994).
RN [14]
RP DISULFIDE BONDS.
RA Sabar M.A., Stockbauer P., Moravsek L., Meloun B.;
RT "Disulfide bonds in human serum albumin.";
RL Collect. Czech. Chem. Commun. 42:564-579(1977).
RN [15]
RP BILIRUBIN-BINDING SITE.
RX MEDLINE=78186630; PubMed=656055;
RA Jacobsen C.;
RT "Lysine residue 240 of human serum albumin is involved in high-
affinity binding of bilirubin.";
RL Biochem. J. 171:453-459(1978).

RN [16]
RP VARIANT CANTERBURY ASN-337.
RX MEDLINE=87157744; PubMed=3828358;
RA Brennan S.O., Herbert P.;
RT "Albumin Canterbury (313 Lys-->Asn). A point mutation in the second
domain of serum albumin.";
RL Biochim. Biophys. Acta 912:191-197(1987).
RN [17]
RP VARIANTS NAG-2 AND NAG-3.
RX MEDLINE=88068523; PubMed=3479777;
RA Takahashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
RA Satoh C., Neel J.V.;
RT "Amino acid substitutions in inherited albumin variants from
American and Japanese populations.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
RN [18]
RP VARIANTS NAG-1; HIR-1; HIR-2 AND TOCHIGI.
RX MEDLINE=89345611; PubMed=2762316;
RA Arai K., Madison J., Huss K., Ishioke N., Satoh C., Fujita M.,
RA Neel J.V., Sakurabayashi I., Putnam F.W.;
RT "Point substitutions in Japanese alloalbumins.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
RN [19]
RP VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
RX MEDLINE=90115905; PubMed=2404284;
RA Arai K., Madison J., Shimizu A., Putnam F.W.;
RT "Point substitutions in albumin genetic variants from Asia.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
RN [20]
RP DESCRIPTION OF VARIANT REDHILL.
RX MEDLINE=90115852; PubMed=2104980;
RA Brennan S.O., Wyles T., Peach R.J., Donaldson D., George P.M.;
RT "Albumin Redhill (-1 Arg, 320 Ala->Thr): a glycoprotein variant of
human serum albumin whose precursor has an aberrant signal peptidase
cleavage site.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
RN [21]
RP VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106.
RX MEDLINE=91062352; PubMed=2247440;
RA Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
RA Watkins S., Putnam F.W.;
RT "Mutations in genetic variants of human serum albumin found in
Italy.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
RN [22]
RP VARIANT VENEZIA.
RX MEDLINE=91296740; PubMed=2068071;
RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
RA Minchiotti L., Putnam F.W.;
RT "A donor splice mutation and a single-base deletion produce two
carboxyl-terminal variants of human serum albumin.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
RN [23]
RP VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23;
RX KOMAGOME-2 ARG-152 AND KOMAGOME-1 GLU-396.
RX MEDLINE=92052189; PubMed=1946412;
RA Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E.,
RA Matsuda Y.-I., Amaki I., Putnam F.W.;
RT "Genetic variants of serum albumin in Americans and Japanese.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
RN [24]
RP VARIANT CASEBROOK ASN-518.
RX MEDLINE=91316157; PubMed=1859851;
RA Peach R.J., Brennan S.O.;
RT "Structural characterization of a glycoprotein variant of human serum
albumin: albumin Casebrook (494 Asp->Asn).";
RL Biochim. Biophys. Acta 1097:49-54(1991).
RN [25]
RP VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
RX MEDLINE=92190239; PubMed=1347703;
RA Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
RA Rochu D., Porta F.;
RT "Two alloalbumins with identical electrophoretic mobility are produced

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CC CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC CC -1- SIMILARITY: Contains 3 albumin domains.
CC CC -----
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CC CC -----
CC DR EMBL: V01222; CAA24532.1; -.
CC DR PIR: A93872; ABRTS.
CC DR HSPG; P02768; IE7B.
CC DR InterPro: IPR000264; Serum_albumin.
CC DR Pfam: PF00273; transport_prot; 3.
CC DR PRINTS: PR00802; SERUMALBUMIN
CC DR ProDom: PD002486; Serum_albumin; 1.
CC DR SMART: SMO0103; ALBUMIN; 3.
CC DR PROSITE; PS00212; ALBUMIN; 3.
CC KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
CC CC SIGNAL      1      18
CC FT PROPEP    19     24
CC FT CHAIN     25     608
CC FT PEPTIDE   166    174
CC FT DOMAIN    25     205
CC FT DOMAIN    212    397
CC FT DOMAIN    404    595
CC FT METAL     27     27
CC FT DISULFID  77     86
CC FT DISULFID  99    115
CC FT DISULFID 114    125
CC FT DISULFID 148    193
CC FT DISULFID 192    201
CC FT DISULFID 224    270
CC FT DISULFID 269    277
CC FT DISULFID 289    303
CC FT DISULFID 302    313
CC FT DISULFID 340    385
CC FT DISULFID 384    393
CC FT DISULFID 416    462
CC FT DISULFID 461    472
CC FT DISULFID 485    501
CC FT DISULFID 500    511
CC FT DISULFID 538    583
CC FT DISULFID 582    591
CC FT VARIANT   262    262
CC FT CONFLICT  174    174
CC SQ SEQUENCE  608 AA; 68718 MW; 5BB497A28241LAB7 CRC64;
Query Match          98.3%; Score 57; DB 1; Length 608;
Best Local Similarity 90.9%; Pred. No. 0.0022;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 AHKSEVAHRFK 11
Db       26 AHKSEIAHRFK 36
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RESULT 3
ALBU_MACMU STANDARD; PRT; 600 AA.
ID ALBU_MACMU Q28522;
AC AC Q28522;
DT DT 01-NOV-1997 (Rel. 35, Created)
DT DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DE Serum albumin precursor (Fragment).
GN GN ALB.
OS OS Macaca mulatta (Rhesus macaque).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC OC Cercopithecinae; Macaca.
OX OX NCBI_TaxId=9544;
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RN  SEQUENCE FROM N.A.
RP  MEDLINE=93211971; PubMed=8460152;
RA  Watkins S.A., Sakamoto Y., Madison J.M., Davis E.M., Smith D.G.,
RT  Dwulet J., Putnam F.W.;
RT  *cDNA and protein sequence of polymorphic macaque albumins that differ
RT  in bilirubin binding.*;
RL  Proc. Natl. Acad. Sci. U.S.A. 90:2409-2413(1993).
CC  -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC  binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC  hormones, bilirubin and drugs. Its main function is the regulation
CC  of the colloidal osmotic pressure of blood.
CC  -1- TISSUE SPECIFICITY: Plasma.
CC  -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC  -1- SIMILARITY: Contains 3 albumin domains.
CC  -----
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CC  -----
CC  EMBL; M90463; AAA36906.1; -.
CC  DR  PIR; A47391; A47391.
CC  DR  HSP; P02768; IE7B.
CC  DR  InterPro: IPR000264; Serum_albumin.
CC  DR  Pfam; PF00273; transport_prot; 3.
CC  DR  PRINTS; PR00802; SERUMALBUMIN.
CC  DR  PRODOM; PD002486; Serum_albumin; 1.
CC  DR  SMART; SM00103; ALBUMIN; 3.
CC  DR  PROSITE; PS00212; ALBUMIN; 3.
CC  KW  Metal-binding; Lipid-binding; Repeat; Signal; Copper.
FT  NON_TER 1 1
FT  SIGNAL <1 10 BY SIMILARITY.
FT  FT PROPEP 11 16 BY SIMILARITY.
FT  FT CHAIN 17 16 SERUM ALBUMIN.
FT  FT DOMAIN 17 197 ALBUMIN 1.
FT  FT DOMAIN 204 389 ALBUMIN 2.
FT  FT DOMAIN 396 587 ALBUMIN 3.
FT  FT METAL 19 19 COPPER (BY SIMILARITY).
FT  FT BINDING 256 256 BILIRUBIN (POTENTIAL).
FT  FT DISULFID 69 78 BY SIMILARITY.
FT  FT DISULFID 91 107 BY SIMILARITY.
FT  FT DISULFID 106 117 BY SIMILARITY.
FT  FT DISULFID 140 185 BY SIMILARITY.
FT  FT DISULFID 184 193 BY SIMILARITY.
FT  FT DISULFID 216 262 BY SIMILARITY.
FT  FT DISULFID 261 269 BY SIMILARITY.
FT  FT DISULFID 281 295 BY SIMILARITY.
FT  FT DISULFID 294 305 BY SIMILARITY.
FT  FT DISULFID 332 377 BY SIMILARITY.
FT  FT DISULFID 376 385 BY SIMILARITY.
FT  FT DISULFID 408 454 BY SIMILARITY.
FT  FT DISULFID 453 464 BY SIMILARITY.
FT  FT DISULFID 477 493 BY SIMILARITY.
FT  FT DISULFID 492 503 BY SIMILARITY.
FT  FT DISULFID 530 575 BY SIMILARITY.
FT  FT DISULFID 574 583 BY SIMILARITY.
SQ  SEQUENCE 600 AA; 67880 MW; B45C871A670E740B CRC64;

Query Match 93.1%; Score 54; DB 1; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HKSEVAHRFK 11
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Db 19 HKSEVAHRFK 28

RESULT 4

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ALBU_MERUN STANDARD; PRT; 609 AA.
ID AC Q35030;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OC NCBI_TaxID=10047;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=MGS IDR: TISSUE=Liver;
RC MEDLINE=98116663; PubMed=9455485;
RA Yoshida K., Seto-Onihama A., Sinozawa H.;
RT *Sequencing of cDNA encoding serum albumin and its extrahepatic
RT synthesis in the Mongolian gerbil, Meriones unguiculatus.*;
RL DNA Res. 4:351-354(1997).
CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -1- SIMILARITY: Contains 3 albumin domains.
CC -----
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CC -----
CC EMBL; AB006197; BAA21765.1; -.
CC DR  PIR; JC5838; JC5838.
CC DR  HSP; P02768; IE7B.
CC DR  InterPro: IPR000264; Serum_albumin.
CC DR  Pfam; PF00273; transport_prot; 3.
CC DR  PRINTS; PR00802; SERUMALBUMIN.
CC DR  PRODOM; PD002486; Serum_albumin; 1.
CC DR  SMART; SM00103; ALBUMIN; 3.
CC DR  PROSITE; PS00212; ALBUMIN; 3.
CC KW  Metal-binding; Lipid-binding; Repeat; Signal; Copper.
FT  SIGNAL 1 18 BY SIMILARITY.
FT  FT PROPEP 19 24 BY SIMILARITY.
FT  FT CHAIN 25 609 SERUM ALBUMIN.
FT  FT DOMAIN 25 206 ALBUMIN 1.
FT  FT DOMAIN 213 398 ALBUMIN 2.
FT  FT DOMAIN 405 596 ALBUMIN 3.
FT  FT METAL 28 28 COPPER.
FT  FT DISULFID 78 87 BY SIMILARITY.
FT  FT DISULFID 100 116 BY SIMILARITY.
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FT  FT DISULFID 149 194 BY SIMILARITY.
FT  FT DISULFID 193 202 BY SIMILARITY.
FT  FT DISULFID 225 271 BY SIMILARITY.
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FT  FT DISULFID 341 386 BY SIMILARITY.
FT  FT DISULFID 385 394 BY SIMILARITY.
FT  FT DISULFID 417 463 BY SIMILARITY.
FT  FT DISULFID 462 473 BY SIMILARITY.
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FT  FT DISULFID 501 512 BY SIMILARITY.
FT  FT DISULFID 539 584 BY SIMILARITY.
FT  FT DISULFID 583 592 BY SIMILARITY.
SQ  SEQUENCE 609 AA; 68940 MW; 9CA5F97F67E1A48 CRC64;

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Query Match          93.1%; Score 54; DB 1; Length 609;
Best Local Similarity 81.8%; Pred. No. 0.0082;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
Db 27 AHKSEIAHRYK 37

RESULT 5
ALBU_BOVIN
ID ALBU_BOVIN STANDARD; PRT; 607 AA.
AC P02769; Q02787;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Bos d 6).
GN ALB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Holowachuk E.W., Stoltenborg J.K., Reed R.G., Peters T. Jr.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT THR-214.
RC TISSUE=Liver;
RA Barry T., Power S., Gannon F.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Hilger C., Grigioni F., de Beaufort C., Michel G., Hentges F.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT THR-214.
RA Wu H.T., Huang M.C.;
RL "The complete cDNA sequence of bovine serum albumin.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1-32.
RX MEDLINE=80024278; PubMed=488109;
RA McGilivray R.T.A., Chung D.W., Davie E.W.;
RT "Biosynthesis of bovine plasma proteins in a cell-free system. Amino-
terminal sequence of prealbumin.";
RL Eur. J. Biochem. 98:477-485(1979).
RN [6]
RP SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214.
RA Brown J.R.;
RT "Structure of bovine serum albumin.";
RL Fed. Proc. 34:591-591(1975).
RN [7]
RP REVISIONS TO 190-195.
RA Brown J.R.;
RL Submitted (APR-1975) to the PIR data bank.
RN [8]
RP SEQUENCE OF 402-433.
RX MEDLINE=82023364; PubMed=7283978;
RA Reed R.G., Putnam F.W., Peters T. Jr.;
RT "Sequence of residues 400-403 of bovine serum albumin.";
RL Biochem. J. 191:867-868(1980).
RN [9]
RP SEQUENCE OF 19-28.
RX MEDLINE=77134075; PubMed=843354;
RA Patterson J.E., Geller D.M.;
RT "Bovine microsomal albumin: amino terminal sequence of bovine
proalbumin.";
RL Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
RN [10]

SEQUENCE, AND REVISIONS TO 118-119 AND 180.
RX MEDLINE=91083649; PubMed=2260975;
RA Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
RT "Rapid confirmation and revision of the primary structure of bovine
serum albumin by ESIMS and Frit-FAB LC/MS.";
RL Biochem. Biophys. Res. Commun. 173:639-646(1990).
RN [11]
RP SEQUENCE OF 25-41.
RX MEDLINE=88267456; PubMed=3389500;
RA Hsieh J.C., Lin F.P., Tam M.F.;
RT "Electroblotting onto glass-fiber filter from an analytical
isoelectrofocusing gel: a preparative method for isolating proteins
for N-terminal microsequencing.";
RL Anal. Biochem. 170:1-8(1988).
RN [12]
RP SEQUENCE OF 437-451.
RA Vilbois F.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
RN [13]
RP DISULFIDE BONDS.
RA Brown J.R.;
RT "Structure of serum albumin: disulfide bridges.";
RL Fed. Proc. 33:1389-1389(1974).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
hormones, bilirubin and drugs. Its main function is the regulation
of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -!- SIMILARITY: Contains 3 albumin domains.
CC
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M73993; AAA51411.1; -
CC EMBL; X58989; CAA41735.1; -
CC EMBL; Y17769; CAA76847.1; -
CC EMBL; AF542068; AAN17824.1; -
CC HSSP; P02768; 1E7B.
CC InterPro; IPR000264; Serum albumin.
CC Pfam; PF00273; transport_prot; 3.
CC PRINTS; PR00802; SERUMALBUMIN.
CC ProDom; PD002486; Serum-albumin; 1.
CC SMART; SM00103; ALBUMIN; 3.
CC PROSITE; PS00212; ALBUMIN; 3.
CC Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen;
KW Polymorphism.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 607 SERUM ALBUMIN.
FT DOMAIN 25 204 ALBUMIN 1.
FT DOMAIN 211 396 ALBUMIN 2.
FT DOMAIN 403 594 ALBUMIN 3.
FT METAL 27 27 COPPER (BY SIMILARITY).
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 147 192
FT DISULFID 191 200
FT DISULFID 223 269
FT DISULFID 268 276
FT DISULFID 288 302
FT DISULFID 301 312
FT DISULFID 339 384
FT DISULFID 383 392
FT DISULFID 415 461
FT DISULFID 460 471

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FT DISULFID 484 500
 FT DISULFID 499 510
 FT DISULFID 537 582
 FT DISULFID 581 590
 FT VARIANT 214 214
 FT CONFLICT 302 302
 FT CONFLICT 304 305
 FT CONFLICT 324 324
 FT CONFLICT 324 395
 FT CONFLICT 394 437
 FT CONFLICT 437 494
 FT CONFLICT 493 494
 SQ SEQUENCE 607 AA; 69293 MW; 39167DFE768585D4 CRC64;

Query Match 91.4%; Score 53; DB 1; Length 607;
 Best Local Similarity 90.0%; Pred. No. 0.013;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRFK 11
 |||||:|||||
 Db 27 HKSEIAHRFK 36

RESULT 6

ALBU_RABIT
 ID ALBU_RABIT STANDARD; PRT; 608 AA.
 AC P49065:
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-New Zealand white; TISSUE=Liver;
 RA Sheffield W.P., Syed S., Schuyler P.D.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 hormones, bilirubin and drugs. Its main function is the regulation
 of the colloidal osmotic pressure of blood.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma.
 CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -!- SIMILARITY: Contains 3 albumin domains.

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 or send an email to license@sib-sib.ch).

DR EMBL: U18344; AAB58347.1; -.
 DR HSP: P02768; IEB7.
 DR InterPro: IPR000264; Serum_albumin.
 DR Pfam: PF00273; transport_prot; 3.
 DR PRINTS: PD00802; SERUMALBUMIN.
 DR ProDom: PD002486; Serum_albumin; 1.
 DR SMART: SM00103; ALBUMIN; 3.
 DR PROSITE: PS00212; ALBUMIN; 3.
 DR Metal-binding; Lipid-binding; Repeat; Signal; Copper.
 KW SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 608
 FT DOMAIN 25 205
 FT DOMAIN 212 397
 FT DOMAIN 404 595
 FT METAL 27 27

FT DISULFID 77 86
 FT DISULFID 99 115
 FT DISULFID 114 125
 FT DISULFID 148 193
 FT DISULFID 192 201
 FT DISULFID 224 270
 FT DISULFID 269 277
 FT DISULFID 289 303
 FT DISULFID 302 313
 FT DISULFID 340 385
 FT DISULFID 384 393
 FT DISULFID 416 461
 FT DISULFID 461 472
 FT DISULFID 485 501
 FT DISULFID 500 511
 FT DISULFID 538 583
 FT DISULFID 582 591
 SQ SEQUENCE 608 AA; 68914 MW; CF5E92647AAFE9A2 CRC64;

Query Match 89.7%; Score 52; DB 1; Length 608;
 Best Local Similarity 90.0%; Pred. No. 0.02;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 10
 |||||:|||||
 Db 26 AHKSEIAHRF 35

RESULT 7

ALBU_MOUSE
 ID ALBU_MOUSE STANDARD; PRT; 608 AA.
 AC P07724; Q61802;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serum albumin precursor.
 GN ALB OR ALB1 OR ALB-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6J; TISSUE=Tongue;
 RX MEDLINE-21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Rustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).

RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE OF 99-516 FROM N.A.
 RX MEDLINE-88216123; PubMed-2452956;

RA Minghetti P.P., Law S.W., Dugaiczak A.;
RT "The rate of molecular evolution of alpha-fetoprotein approaches that
RL of pseudogenes.";
RN Mol. Biol. Evol. 2:347-358(1985).
RP [4]
RC SEQUENCE OF 477-551 FROM N.A.
RX MEDLINE=90269606; PubMed=1971802;
RA Bocaccio C., Deschattre J., Meunier-Rotival M.;
RT "Empty and occupied insertion site of the truncated LINE-1 repeat
RL located in the mouse serum albumin-encoding gene.";
RN Gene 88:181-186(1990).
RP [5]
RC SEQUENCE OF 25-44.
RX TISSUE=Liver;
RA Giometti C.S., Taylor J., Tollaksen S.L.;
RT "Mouse liver protein database: a catalog of proteins detected by two-
RN dimensional gel electrophoresis.";
RL Electrophoresis 13:970-991(1992).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: Contains 3 albumin domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: A011413; CAA09617.1; -
CC EMBL: M16111; AAA37190.1; -
CC EMBL: X13060; CAA31458.1; -
CC EMBL: AK010025; BAB26650.1; -
CC PIR: A05139; A05139.
CC HSP: P02768; 1E7B.
CC SWISS-2DPAGE: P07724; MOUSE.
CC MGD: MGI:87991; Alb1.
CC InterPro: IPR000264; Serum_albumin.
CC Pfam: PF00273; transport_prot; 3.
CC PRINTS: PR00802; SERUMALBUMIN.
CC ProDom: PD002486; Serum_albumin; 1.
CC SMART: SM00103; ALBUMIN; 3.
CC PROSITE: PS00212; ALBUMIN; 3.
CC Metal-binding; Lipid-binding; Repeat; Signal; Copper.
KW SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24
FT CHAIN 25 608 SERUM ALBUMIN.
FT DOMAIN 25 205 ALBUMIN 1.
FT DOMAIN 212 397 ALBUMIN 2.
FT DOMAIN 404 595 ALBUMIN 3.
FT METAL 27 27 COPPER.
FT DISULFID 27 27 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.

FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT CONFLICT 27 27 H -> D (IN REF. 5).
FT CONFLICT 33 33 H -> D (IN REF. 5).
FT CONFLICT 41 41 Q -> I (IN REF. 5).
SQ SEQUENCE 608 AA; 68692 MW; 292F7C7EED3A61B4 CRC64;

Query Match 84.5%; Score 49; DB 1; Length 608;
Best Local Similarity 80.0%; Pred. No. 0.075;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRP 10
DB 26 AHKSEIAHRY 35
|||||:

RESULT 8
ALBU_HORSE STANDARD; PRT; 607 AA.
AC P35747;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor.
GN ALB.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RC TISSUE=Liver;
RX MEDLINE=93345495; PubMed=8344282;
RA Ho J.X., Holowachuk E.W., Norton E.J., Twigg P.D., Carter D.C.;
RT "X-ray and primary structure of horse serum albumin (Equus caballus)
at 0.27-nm resolution.";
RL Eur. J. Biochem. 215:205-212(1993).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -!- SIMILARITY: Contains 3 albumin domains.
CC
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CC
CC EMBL: X74045; CAA52194.1; -
CC PIR: S34053; ABHOS.
CC HSP: P02768; 1E7B.
CC InterPro: IPR000264; Serum_albumin.
CC Pfam: PF00273; transport_prot; 3.
CC PRINTS: PR00802; SERUMALBUMIN.
CC ProDom: PD002486; Serum_albumin; 1.
CC SMART: SM00103; ALBUMIN; 3.
CC PROSITE: PS00212; ALBUMIN; 3.
CC Metal-binding; Lipid-binding; Repeat; Signal; Copper.
KW SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24 BY SIMILARITY.
FT CHAIN 25 607 SERUM ALBUMIN.
FT DOMAIN 25 204 ALBUMIN 1.
FT DOMAIN 211 396 ALBUMIN 2.
FT DOMAIN 403 594 ALBUMIN 3.
FT METAL 27 27 COPPER (BY SIMILARITY).
FT DISULFID 77 86


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RC TISSUE=Liver;
RA Cassidy A.I., Salkild C.K., Baverstock P., Wallace J.C.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=83161037; PubMed=6187737;
RA Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.;
RL "The 5' noncoding and flanking regions of the avian very low density
RT apolipoprotein II and serum albumin genes. Homologies with the egg
RL white protein genes.;"
RL J. Biol. Chem. 258:4556-4564(1983).
RN [3]
RP SEQUENCE OF 19-30.
RX MEDLINE=78019943; PubMed=911327;
RA Rosen A.M., Geller D.M.;
RL "Chicken microsomal albumin: amino terminal sequence of chicken
RT proalbumin.;"
RL Biochem. Biophys. Res. Commun. 78:1060-1066(1977).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC -!- SIMILARITY: Contains 3 albumin domains.
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CC -----
DR EMBL; X60688; CAA43098.1; -.
DR EMBL; V00381; CAA23680.1; -.
DR PIR; S15571; ABCHS.
DR HSP; P02768; IE7B.
DR InterPro; IPR000264; Serum_albumin.
DR PRINTS; PR00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Metal-binding; Lipid-binding; Repeat; Signal; Copper.
FT SIGNAL 1 18
FT PROPEP 19 23
FT CHAIN 24 615 SERUM ALBUMIN.
FT DOMAIN 24 209 ALBUMIN 1.
FT DOMAIN 216 401 ALBUMIN 2.
FT DOMAIN 408 599 ALBUMIN 3.
FT METAL 30 30 COPPER (BY SIMILARITY).
FT METAL 80 89 BY SIMILARITY.
FT DISULFID 102 118 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 152 197 BY SIMILARITY.
FT DISULFID 196 205 BY SIMILARITY.
FT DISULFID 228 274 BY SIMILARITY.
FT DISULFID 273 281 BY SIMILARITY.
FT DISULFID 306 317 BY SIMILARITY.
FT DISULFID 344 389 BY SIMILARITY.
FT DISULFID 388 397 BY SIMILARITY.
FT DISULFID 420 466 BY SIMILARITY.
FT DISULFID 465 476 BY SIMILARITY.
FT DISULFID 489 505 BY SIMILARITY.
FT DISULFID 504 515 BY SIMILARITY.
FT DISULFID 542 587 BY SIMILARITY.
FT DISULFID 586 595 BY SIMILARITY.
FT CARBOHYD 500 500 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 24 24 F -> M (IN REF. 3).
SQ SEQUENCE 615 AA; 69918 MW; E59E4BBAC066C6 CRC64;

Query Match 77.6%; Score 45; DB 1; Length 615;
Best Local Similarity 77.8%; Pred. No. 0.45;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
DB 30 HKSEIAHRY 38
|||||:
|||||:

RESULT 13
ALBU_TRASC STANDARD; PRT; 40 AA.
ID ALBU_TRASC
AC P81188;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 67 kDa serum albumin (Alb-1) (Fragment).
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoida; Emydidae; Trachemys.
OX NCBI_TaxID=34903;
RN [1]
RP SEQUENCE.
RX MEDLINE=98103404; PubMed=9440230;
RA Brown M.A., Chambers G.K., Licht P.;
RT "Purification and partial amino acid sequences of two distinct
RL albumins from turtle plasma.;"
RL Comp. Biochem. Physiol. 118B:367-374(1997).
RN [2]
RP SEQUENCE OF 1-8.
RX MEDLINE=95309661; PubMed=7789749;
RA Selcer K.W., Palmer B.D.;
RT "Estrogen downregulation of albumin and a 170-kDa serum protein in
RL the turtle, Trachemys scripta.;"
RL Gen. Comp. Endocrinol. 97:340-352(1995).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- MISCELLANEOUS: IN THE RED-EARED SLIDER TURTLE, THERE ARE TWO FORMS
CC OF ALBUMIN, ALB-1 AND ALB-2.
CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
CC HSP; P02768; IE7B.
CC InterPro; IPR000264; Serum_albumin.
CC Pfam; PF00273; transport_prot; 1.
CC PROSITE; PS00212; ALBUMIN; PARTIAL.
KW Metal-binding; Lipid-binding; Copper.
FT METAL 4 4 COPPER (BY SIMILARITY).
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4682 MW; 5FAC9E49E2789BB0 CRC64;

Query Match 75.9%; Score 44; DB 1; Length 40;
Best Local Similarity 77.8%; Pred. No. 0.037;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
DB 4 HKSEIVHRF 12
|||||:
|||||:

RESULT 14
ALBU_CANFA STANDARD; PRT; 608 AA.
ID ALBU_CANFA
AC P49822; O77705; Q9TSZ4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum albumin precursor (Allergen Can f 3).
GN ALB.
OS Canis familiaris (Dog).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Beagle; TISSUE=Liver;
 RA Hilger C.; Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20148667; PubMed=10669848;
 RA Pandjaitan B., Swoboda I., Brandesky-Pichler F., Rumpold H.,
 RA Valenta R., Spitzauer S.;
 RT "Escherichia coli expression and purification of recombinant dog
 RT albumin, a cross-reactive animal allergen.";
 RL J. Allergy Clin. Immunol. 105:279-285(2000).
 RN [3]
 RP SEQUENCE OF 25-48.
 RX MEDLINE=75011422; PubMed=4414013;
 RA Dixon J.W., Sarkar B.;
 RT "Isolation, amino acid sequence and copper(II)-binding properties of
 RT peptide (1-24) of dog serum albumin.";
 RL J. Biol. Chem. 249:5872-5877(1974).
 RN [4]
 RP SEQUENCE OF 25-38.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 RN [5]
 RP SEQUENCE OF 215-478 FROM N.A.
 RX TISSUE=Salivary gland;
 RA Spitzauer S., Schweiger C., Sperr W.R., Pandjaitan B., Valent P.,
 RA Muehl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
 RT "Molecular characterization of dog albumin as a cross-reactive
 RT allergen.";
 RL J. Allergy Clin. Immunol. 93:614-627(1994).
 CC -|- FUNCTION: Serum albumin, the main protein of plasma, has a good
 CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 CC hormones, bilirubin and drugs. Its main function is the regulation
 CC of the colloidal osmotic pressure of blood.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Plasma.
 CC -|- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
 CC -|- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
 CC -----
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 CC -----
 CC EMBL; AJ133489; CAB64867.1; -;
 DR EMBL; Y17737; CAA76841.1; -;
 DR EMBL; S72946; AAB30434.1; -;
 DR HSP; P02768; 1E7B.
 DR HSC-2DPAGE; P49822; DOG.
 DR InterPro; IPR000264; Serum_albumin.
 DR Pfam; PF00273; transprot_prot; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum_albumin; 1.
 DR SMART; SM00103; ALBUMIN; 3.
 DR PROSITE; PS00212; ALBUMIN; 3.
 KW Metal-binding; Lipid-binding; Repeat; Signal; Copper; Allergen.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 24
 FT CHAIN 25 608 SERUM ALBUMIN.

FT DOMAIN 25 205 ALBUMIN 1.
 FT FT 212 337 ALBUMIN 2.
 FT FT 404 595 ALBUMIN 3.
 FT FT 27 27 COPPER (BY SIMILARITY).
 FT FT 77 86 BY SIMILARITY.
 FT FT 99 115 BY SIMILARITY.
 FT FT 114 125 BY SIMILARITY.
 FT FT 148 193 BY SIMILARITY.
 FT FT 192 201 BY SIMILARITY.
 FT FT 224 270 BY SIMILARITY.
 FT FT 269 277 BY SIMILARITY.
 FT FT 289 303 BY SIMILARITY.
 FT FT 302 313 BY SIMILARITY.
 FT FT 340 385 BY SIMILARITY.
 FT FT 384 393 BY SIMILARITY.
 FT FT 416 462 BY SIMILARITY.
 FT FT 461 472 BY SIMILARITY.
 FT FT 485 501 BY SIMILARITY.
 FT FT 500 511 BY SIMILARITY.
 FT FT 538 583 BY SIMILARITY.
 FT FT 582 591 BY SIMILARITY.
 FT FT 1 26 MKWVFISLFLESSAYSRLVREA -> MDT (IN
 FT REF. 2).
 FT CONFLICT 146 146 A -> R (IN REF. 2).
 FT CONFLICT 206 206 I -> T (IN REF. 2).
 FT CONFLICT 349 349 V -> A (IN REF. 2).
 FT CONFLICT 359 359 S -> A (IN REF. 1).
 FT CONFLICT 448 448 V -> VV (IN REF. 5).
 FT CONFLICT 474 474 D -> E (IN REF. 1).
 SQ SEQUENCE 608 AA; 68606 MW; 3CFIC8FF7DD8FC06 CRC64;
 Query Match 74.1%; Score 43; DB 1; Length 608;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AHKSEVAHRF 10
 Db 26 AYKSEIHAHY 35
 RESULT 15
 RBMC_MOUSE STANDARD; PRT; 1002 AA.
 ID RBMC_MOUSE Q8R4X3; Q8R302; Q9CS80;
 AC Q8R4X3; Q8R302; Q9CS80;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE RNA-binding protein 12 (RNA binding motif protein 12) (SH3/WW domain
 DE anchor protein in the nucleus) (SWAN).
 GN RBM12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang C.-H.;
 RT "Identification of SWAN as a novel hnRNP-like adaptor protein with
 RT multiple domains and broadly expressed in mammalian tissues.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo, and Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Velardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE OF 116-1002 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
CC -----
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CC -----
DR EMBL; AF345334; AAL83754.1; -;
DR EMBL; AF393215; AAM73683.1; -;
DR EMBL; AF393216; AAM73684.1; -;
DR EMBL; AK017591; BAB30825.1; -;
DR EMBL; AK029180; BAC26338.1; -;
DR EMBL; AK035014; BAC28911.1; -;
DR EMBL; AK080772; BAC38017.1; -;
DR EMBL; BC026891; AAH26891.1; ALT_INIT.
DR EMBL; BC027810; AAH27810.1; ALT_INIT.
DR MGD; MGI:1922960; Rbm12.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; Rrm; 3.
DR SMART; SM00360; RRM; 4.
DR PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
DR PROSITE; PS0102; RRM; 3.
KW Nuclear protein; RNA-binding; Repeat.
FT DOMAIN 159 256
FT 256 PRO-RICH.
FT 304 RNA-BINDING (RRM) 1.
FT 379

FT DOMAIN 430 507 RNA-BINDING (RRM) 2.
FT DOMAIN 644 925 PRO-RICH.
FT DOMAIN 656 924 GLY-RICH.
FT DOMAIN 926 1002 RNA-BINDING (RRM) 3.
FT CONFLICT 122 122 I -> T (IN REF. 1).
FT CONFLICT 572 572 N -> S (IN REF. 2).
FT BAC26338/BAC28911/BAC38017).
FT G -> S (IN REF. 2; BAC28911).
FT G -> S (IN REF. 2; BAB30825).
FT G -> C (IN REF. 2; BAB30825).
FT MISSING (IN REF. 2).
FT BAB30825/BAC28911/BAC38017).
FT MISSING (IN REF. 2; BAC26338).
FT G -> GGG (IN REF. 1).
FT V -> A (IN REF. 1).
FT V -> G (IN REF. 1).
FT E -> D (IN REF. 1).
FT AP -> G (IN REF. 1).
FT P -> L (IN REF. 1).
SQ SEQUENCE 1002 AA; 103724 MW; 5B560124232F6A49 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 1002;
Best Local Similarity 72.7%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREF 11
||||| |||
Db 598 AHKSEHLHRKK 608

Search completed: August 29, 2003, 14:26:59
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:23:55 ; Search time 95 seconds
(without alignments)
29.880 Million cell updates/sec

Title: US-09-845-726a-1_COPY_2_l2

Perfect score: 58
Sequence: 1 AHKSEVAHRFK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_protist.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	21	11 Q9QVAL	Q9qval rattus sp.
2	58	100.0	396	4 Q8IUK7	Q8Iuk7 homo sapien
3	57	98.3	20	11 Q9QUX8	Q9qux8 rattus sp.
4	57	98.3	608	5 Q95VB7	Q95vb7 schistosoma
5	53	91.4	20	2 Q9R4X7	Q9r4x7 mycobacteri
6	52	89.7	40	6 Q9TRA5	Q9tra5 oryctolagus
7	49	84.5	205	11 Q8CG74	Q8cg74 mus musculu
8	49	84.5	608	11 Q8C7H3	Q8c7h3 mus musculu
9	45	77.6	30	13 Q9PRW0	Q9prw0 struthio ca
10	43	74.1	17	6 Q9TR98	Q9tr98 canis fami
11	43	74.1	20	6 Q9TQZ6	Q9tqz6 macaca fasc
12	39.5	68.1	201	16 Q9PQK4	Q9pqk4 ureaplasma
13	38	65.5	152	16 Q8EOM2	Q8eqm2 oceanobacil
14	38	65.5	3209	5 Q8I5D0	Q8I5d0 plasmodium
15	37	63.8	93	16 Q8YNI1	Q8yni1 anabaena sp
16	37	63.8	253	16 Q98N78	Q98nt8 rhizobium l

17	63.8	37	408	11	Q9CS80	Q9cs80 mus musculu
18	63.8	37	841	11	Q8R302	Q8r302 mus musculu
19	63.8	37	876	17	Q8PSW8	Q8psw8 methanosarc
20	63.8	37	1003	11	Q8R4X3	Q8r4x3 mus musculu
21	62.1	36	53	12	Q11370	Q11370 molluscum c
22	62.1	36	117	12	Q98304	Q98304 molluscum c
23	62.1	36	285	16	Q8PFE6	Q8pfe6 xanthomonas
24	62.1	36	463	16	Q8FW73	Q8fw73 brucella su
25	62.1	36	489	16	Q8YC53	Q8yc53 brucella me
26	62.1	36	537	6	Q9MZU5	Q9mzu5 sus scrofa
27	62.1	36	1096	10	Q9XE24	Q9xe24 oryza sativ
28	62.1	36	1827	5	Q20042	Q20042 caenorhabdi
29	62.1	36	1885	5	Q95QG9	Q95qg9 caenorhabdi
30	62.1	36	1898	5	Q95OH0	Q95oh0 caenorhabdi
31	60.3	35	172	4	Q9BYN1	Q9byn1 homo sapien
32	60.3	35	194	4	Q9BY32	Q9by32 homo sapien
33	60.3	35	194	4	Q9H3H8	Q9h3h8 homo sapien
34	60.3	35	194	4	Q14878	Q14878 homo sapien
35	60.3	35	313	3	Q8J179	Q8j179 emericella
36	60.3	35	315	16	Q8E511	Q8e511 streptococ
37	60.3	35	320	10	Q9CAH5	Q9cah5 arabidopsis
38	60.3	35	333	2	Q54274	Q54274 streptomyc
39	60.3	35	414	2	Q32383	Q32383 streptomyc
40	60.3	35	513	17	Q8PZM0	Q8pzm0 methanosarc
41	60.3	35	672	16	Q9KQV0	Q9kgv0 vibrio chol
42	60.3	35	969	5	Q27502	Q27502 caenorhabdi
43	60.3	35	1104	13	Q9W6R6	Q9w6r6 fugu rubrip
44	60.3	35	1197	11	Q921M6	Q921m6 mus musculu
45	60.3	35	1295	4	Q9P2R8	Q9p2r8 homo sapien

ALIGNMENTS

RESULT 1

Q9QVAL PRELIMINARY; PRT; 21 AA.
AC Q9QVAL;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 49 kDa protein (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=93105636; PubMed=1468220;
RA Zhu L., Crouch R.K.;
RT "Albumin in the cornea is oxidized by hydrogen peroxide.";
RL Cornea 11:567-572(1992).
DR HSSP; P02768; 1E7H.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 1.
SQ SEQUENCE 21 AA; 2429 MW; 26134A3D7CE29FAC CRC64;

Query Match 100.0%; Score 58; DB 11; Length 21;
Best Local Similarity 100.0%; Pred No. 0.0001;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11

Db 2 AHKSEVAHRFK 12

RESULT 2

Q8IUK7 PRELIMINARY; PRT; 396 AA.
ID Q8IUK7
AC Q8IUK7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

```

DE Similar to serum albumin precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035969; AAH35969.1; -.
SQ SEQUENCE 396 AA; 45159 MW; 756519C096463A9B CRC64;

Query Match 100.0%; Score 58; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
DB 26 AHKSEVAHREFK 36
|||||:|||||

RESULT 3
ID Q90UX8 PRELIMINARY; PRT; 20 AA.
AC Q90UX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 70 kDa seizure activity-linked albumin-like glycoprotein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96087830; PubMed=8587647;
RA Onozuka M., Imai S., Isobe T., Yen C.T., Watanabe K.;
RT "Purification and characterization of a novel 70-kDa brain protein
RT associated with seizure activities.";
RL Neurochem. Res. 20:901-905(1995).
DR HSP; P02768; IE7H.
SQ SEQUENCE 20 AA; 2381 MW; 53423C0F9F70F7D CRC64;

Query Match 98.3%; Score 57; DB 11; Length 20;
Best Local Similarity 90.9%; Pred. No. 0.00015;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
DB 2 AHKSEIAHREFK 12
|||||:|||||

RESULT 4
ID Q95VB7 PRELIMINARY; PRT; 608 AA.
AC Q95VB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Albumin.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
ON NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RA Osman A., Asahi H., Stadecker M.J., Loverde P.T.;
RT "Albumin precursor homolog is a novel T helper cell immunogenic egg
RT component in murine infection with Schistosoma mansoni.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF418550; AAL08579.1; -.
DR InterPro; IPR000264; Serum_albumin.

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DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PD00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 2.
SQ SEQUENCE 608 AA; 68225 MW; E5EABB28E1C66E54 CRC64;

Query Match 98.3%; Score 57; DB 5; Length 608;
Best Local Similarity 90.9%; Pred. No. 0.0071;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
DB 26 AHKSEIAHREFK 36
|||||:|||||

RESULT 5
ID Q9R4X7 PRELIMINARY; PRT; 20 AA.
AC Q9R4X7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 66 kDa SEROREACTIVE protein/serum albumin homolog (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
ON NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RX MEDLINE=94343500; PubMed=8064836;
RA Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.;
RT "Purification and partial characterisation of a novel 66-kDa
RT seroreactive protein of Mycobacterium tuberculosis H37Rv.";
RL J. Med. Microbiol. 41:173-178(1994).
SQ SEQUENCE 20 AA; 2393 MW; 534A232072870F7D CRC64;

Query Match 91.4%; Score 53; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 0.00098;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHREFK 11
DB 3 HKSEIAHREFK 12
|||||:|||||

RESULT 6
ID Q9TRA5 PRELIMINARY; PRT; 40 AA.
AC Q9TRA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Antagonist protein (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=94359514; PubMed=8078511;
RA Xu A., Narayanan N.;
RT "Purification, amino-terminal sequence and functional properties of a
RT 64 kDa cytosolic protein from heart muscle capable of modulating
RT calcium transport across the sarcoplasmic reticulum in vitro.";
RL Mol. Cell. Biochem. 132:7-14(1994).
DR HSP; P02768; IE7H.
DR InterPro; IPR00264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 1.
SQ SEQUENCE 40 AA; 4694 MW; BA7E0B69C6CE858C CRC64;

Query Match 89.7%; Score 52; DB 6; Length 40;
Best Local Similarity 90.0%; Pred. No. 0.0034;

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Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10
Db 2 AHKSEIAHRF 11

RESULT 7
Q8CG74 Q8CG74 PRELIMINARY; PRT; 205 AA.
AC Q8CG74;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Albumin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvetTACfBr;
RA Van Reeth T., Dreze P.L., Gabant P., Szpirer C., Szpirer J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ277794; CAC81903.1;
FT NON_TER 205
SQ SEQUENCE 205 AA; 23624 MW; 0A982E85C7474BF9 CRC64;

Query Match 84.5%; Score 49; DB 11; Length 205;
Best Local Similarity 80.0%; Pred. No. 0.084;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10
Db 26 AHKSEIAHRF 35

RESULT 8
Q8C7H3 Q8C7H3 PRELIMINARY; PRT; 608 AA.
AC Q8C7H3;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Albumin I.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL: AK050248; BAC34145.1;
SQ SEQUENCE 608 AA; 68722 MW; 292F600ED3A61B4 CRC64;

Query Match 84.5%; Score 49; DB 11; Length 608;
Best Local Similarity 80.0%; Pred. No. 0.28;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10
Db 26 AHKSEIAHRF 35

RESULT 9
Q9PRW0 Q9PRW0 PRELIMINARY; PRT; 30 AA.
ID Q9PRW0

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AC Q9PRW0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha 1-proteinase inhibitor (Fragment).
OS Struthio camelus (Ostrich).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
OC Struthio.
OX NCBI_TaxID=8801;
RN [1]
RP SEQUENCE.
RX MEDLINE=94341467; PubMed=8063009;
RA Kuhn C.R., Naude R.J., Travis J., Oelofsen W.;
RT "The isolation and partial characterization of alpha 1-proteinase
RT inhibitor from the serum of the ostrich (Struthio camelus).";
RL Int. J. Biochem. 26:843-853(1994).
SQ SEQUENCE 30 AA; 3557 MW; 7775AA786BE30AC2 CRC64;

Query Match 77.6%; Score 45; DB 13; Length 30;
Best Local Similarity 77.8%; Pred. No. 0.062;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HKSEVAHRF 10
Db 4 HKSEIAHRF 12

RESULT 10
Q9TR98 Q9TR98 PRELIMINARY; PRT; 17 AA.
AC Q9TR98;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Albumin (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=95007849; PubMed=7923441;
RA Miller M.J., Parmelee D.C., Benjamin T., Sechi S., Dooley K.L.,
RA Kadlubar F.F.;
RT "Plasma proteins as early biomarkers of exposure to carcinogenic
RT aromatic amines";
RL Chem.-Biol. Interact. 93:221-234(1994).
SQ SEQUENCE 17 AA; 2024 MW; ID39F70F7D23B269 CRC64;

Query Match 74.1%; Score 43; DB 6; Length 17;
Best Local Similarity 70.0%; Pred. No. 0.083;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHRF 10
Db 2 AYKSEIAHRF 11

RESULT 11
Q9TQ26 Q9TQ26 PRELIMINARY; PRT; 20 AA.
AC Q9TQ26;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE Albumin (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]

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RP SEQUENCE.
RX MEDLINE=96273610; PubMed=8690030;
RA Nicolas M.G., Fujiki K., Murayama K., Suzuki M.T., Mineki R.,
RA Hayakawa M., Yoshikawa Y., Cho F., Kanai A.;
RT "Studies on the mechanism of early onset macular degeneration in
RT cynomolgus (Macaca fascicularis) monkeys. I. Abnormal concentrations of
RT two proteins in the retina.";
RL Exp. Eye Res. 62:211-219(1996).
SQ SEQUENCE 20 AA; 2411 MW; 5F1A6ABE5918F777 CRC64;

Query Match 74.1%; Score 43; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHR 9
Db |||||
13 HKSEVAHR 20

RESULT 12
Q9POK4 PRELIMINARY; PRT; 201 AA.
ID Q9POK4
AC Q9POK4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein U0287.
GN U0287.
OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Setovar 3;
RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum.";
RL Nature 407:757-762(2000).
DR EMBL; AF02125; AAF30696.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 201 AA; 23872 MW; FD0012911c4BD7E8 CRC64;

Query Match 68.1%; Score 39.5; DB 16; Length 201;
Best Local Similarity 52.6%; Pred. No. 6.6;
Matches 10; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 2 HKS-----EVAHRFK 11
Db |||
79 HKSSSLYLTNDDEVAHRFK 97

RESULT 13
Q8EQM2 PRELIMINARY; PRT; 152 AA.
ID Q8EQM2
AC Q8EQM2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical conserved protein.
GN O81673.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
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RL Nucleic Acids Res. 30:3927-3935(2002).
RX EMBL; AP004598; BAC13629.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 152 AA; 18357 MW; 5FCAF143BF2D0265 CRC64;

Query Match 65.5%; Score 38; DB 16; Length 152;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
Db |||:: |||
19 HKSDLLHRF 27

RESULT 14
Q8I5D0 PRELIMINARY; PRT; 3209 AA.
ID Q8I5D0
AC Q8I5D0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PFL1395C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow J.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA MCPadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser J.C., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014848; AAN36365.1; -.
KW Hypothetical protein.
SQ SEQUENCE 3209 AA; 378904 MW; DA2BBE1737C10873 CRC64;

Query Match 65.5%; Score 38; DB 5; Length 3209;
Best Local Similarity 45.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db ||| |||::: |||
791 SHKDEVSHKYE 801

RESULT 15
Q8YNI1 PRELIMINARY; PRT; 93 AA.
ID Q8YNI1
AC Q8YNI1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Asr4584.
GN ASR4584.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Muraki A.,
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RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003596; BAB76283.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 93 AA; 10516 MW; EA46156FB8729D0E CRC64;

Query Match 63.8%; Score 37; DB 16; Length 93;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 HKSEVAHRF 10
| :| | | | |
Db 46 HAADVVAHRF 54

Search completed: August 29, 2003, 14:28:44
Job time : 98 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:24:05 ; Search time 39 Seconds
(without alignments)
27.125 Million cell updates/sec

Title: US-09-845-726a-1_COPY_2_12

Perfect score: 58

Sequence: 1 AHKSEVAHFK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	609	1 ABHUS	serum albumin prec
2	57	98.3	608	1 ABRTS	serum albumin prec
3	54	93.1	600	2 A47391	serum albumin prec
4	54	93.1	609	2 JC5838	albumin - Mongolia
5	53	91.4	607	1 ABBS	serum albumin prec
6	48	82.8	607	1 ABSHS	serum albumin prec
7	48	82.8	607	1 ABHOS	serum albumin prec
8	48	82.8	608	2 S57632	serum albumin prec
9	47	81.0	605	1 ABPGS	serum albumin prec
10	45	77.6	615	1 ABCHS	serum albumin prec
11	43	74.1	24	2 S29749	serum albumin prec
12	40	69.0	30	2 B61511	serum albumin - do
13	39.5	68.1	201	2 E82910	serum albumin, ml
14	37	63.8	93	2 AH2378	hypothetical prote
15	36	62.1	117	2 T30740	hypothetical prote
16	36	62.1	489	2 AP3594	hypothetical prote
17	36	62.1	719	2 S63392	hypothetical prote
18	36	62.1	1827	2 T16270	probable membrane
19	35	60.3	155	2 G69489	LSU ribosomal prot
20	35	60.3	320	2 D96750	unknown protein F2
21	35	60.3	672	2 H82143	methy-accepting c
22	35	60.3	969	2 T3256	hypothetical prote
23	34	58.6	138	2 C84068	polyribonucleotide
24	34	58.6	156	2 T49921	ribosomal protein-1
25	34	58.6	200	2 C81282	hypothetical prote
26	34	58.6	222	2 A97575	hypothetical prote
27	34	58.6	222	2 A12795	conserved hypothet
28	34	58.6	385	2 C82478	probable integrase
29	34	58.6	391	2 T42407	gephyrin homolog -

RESULT 1

ABHUS

serum albumin precursor [validated] - human

N:Alternate names: preproalbumin

N:Contains: kinetensin

C:Species: Homo sapiens (man)

C>Date: 29-Jul-1981 #sequence revision 31-Jan-1997 #text change 17-Mar-2000

C:Accession: A93743; A93936; I39427; I59286; I59313; G01747; S55314; A91420; S06422;

R:Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; See

Nucleic Acids Res. 9, 6103-6114, 1981

A:Title: The sequence of human serum albumin cDNA and its expression in Escherichia c

A:Reference number: A93743; MUID:82081882; PMID:6171778

A:Accession: A93743

A:Molecule type: mRNA

A:Residues: 1-419, K' 421-609 <LAW>

A:Cross-references: EMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:g28591; PIDN:CA

R:Dugaiczky, A.; Law, S.W.; Dennison, O.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982

A:Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.

A:Reference number: A93936; MUID:82105994; PMID:6275391

A:Accession: A93936

A:Molecule type: mRNA

A:Residues: 1-120, G', 122-609 <DUG>

A:Cross-references: EMBL:V00494; NID:g28589; PIDN:CAA23753.1; PID:g28590

R:Urano, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.

J. Biol. Chem. 261, 3244-3251, 1986

A:Title: The human albumin gene. Characterization of the 5' and 3' flanking regions a

A:Reference number: I39427; MUID:86140099; PMID:2419329

A:Accession: I39427

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-26 <URA>

A:Cross-references: GB:MI3075; NID:g178330; PIDN:AAA51688.1; PID:g553173

R:Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994

A:Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian fami

A:Reference number: I59286; MUID:94181575; PMID:8134387

A:Accession: I59286

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 282-290, 'KSRFDLQ' <WAT>

A:Cross-references: GB:S69199; NID:g546032; PIDN:AAB30282.1; PID:g546033

A>Note: this frame-shift variant, designated albumin Rona, leads to analbuminemia

R:Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putna

Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994

A:Title: Genetic variants of human serum albumin in Italy: point mutants and a carbox

A:Reference number: I59313; MUID:94294404; PMID:8022807

A:Accession: I59313

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 589-590, 'ALPRVRKLLQLVLP' <MAD>

A:Cross-references: GB:S70799; NID:g547231; PIDN:AAB31177.1; PID:g547232

glucose 6-phosphat
probable glucose-6
IMP dehydrogenase
hypothetical 53.4
probable enzyme Y
methionine-tRNA L1
cholesterol monoox
RLR1 protein - yea
hypothetical prote
hypothetical prote
probable oxidoredu
probable oxidoredu
probable membrane

A;Note: this frame-shift variant is designated albumin Bazzano; four additional variants submitted to the EMBL Data Library, March 1995

A;Reference number: G08292

A;Accession: G01747

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-120, 'G', 122-455 <MEN>

A;Cross-references: EMBL:U22961; NID:q763428; PID:g763431

B;Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O. Biochem. J. 308, 321-325, 1995

A;Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast *Kex2*

A;Reference number: S55314; MUID:95275251; PMID:7755581

A;Accession: S55314

A;Molecule type: protein

A;Residues: 19-27 <LED>

R;Meloun, B.; Moravek, L.; Kostka, V. FEBS Lett. 58, 134-137, 1975

A;Title: Complete amino acid sequence of human serum albumin.

A;Reference number: A91420; MUID:76187907; PMID:1225573

A;Accession: A91420

A;Molecule type: protein

A;Residues: 25-117, 'Eq', 120-154, 'Q', 156-193, 'E', 195-387, 'H', 389-390, 'Y', 392-393, 'A', 395-396, 'S', 398-400, 'G', 402-403, 'D', 405-406, 'K', 408-409, 'N', 411-412, 'Q', 414-415, 'E', 417-418, 'D', 420-421, 'G', 423-424, 'K', 426-427, 'E', 429-430, 'D', 432-433, 'G', 435-436, 'K', 438-439, 'E', 441-442, 'Q', 444-445, 'E', 447-448, 'D', 450-451, 'G', 453-454, 'K', 456-457, 'E', 459-460, 'K', 462-463, 'E', 465-466, 'K', 468-469, 'E', 471-472, 'Q', 474-475, 'E', 477-478, 'D', 480-481, 'G', 483-484, 'K', 486-487, 'E', 489-490, 'K', 492-493, 'E', 495-496, 'K', 498-499, 'E', 501-502, 'G', 504-505, 'K', 507-508, 'E', 510-511, 'G', 513-514, 'K', 516-517, 'E', 519-520, 'K', 522-523, 'E', 525-526, 'K', 528-529, 'E', 531-532, 'G', 534-535, 'K', 537-538, 'E', 540-541, 'K', 543-544, 'E', 546-547, 'K', 549-550, 'E', 552-553, 'G', 555-556, 'K', 558-559, 'E', 561-562, 'K', 564-565, 'E', 567-568, 'K', 570-571, 'E', 573-574, 'K', 576-577, 'E', 579-580, 'K', 582-583, 'E', 585-586, 'K', 588-589, 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F;166-174/Product: kinetensin #status experimental <KIP>
F;221-394/Domain: serum albumin repeat homology <SA2>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
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F;214/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 100.0%; Score 58; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
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Db 26 AHKSEVAHRFK 36

RESULT 2
ABRTS
serum albumin precursor - rat
N;Alternate names: preproalbumin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 22-Jun-1999
C;Accession: A93872; A92211; A91946; A91940; C45800; I57621; A03233
R;Sargent, T.D.; Yang, M.; Bonner, J.
Proc. Natl. Acad. Sci. U.S.A. 78, 243-246, 1981
A;Title: Nucleotide sequence of cloned rat serum albumin messenger RNA.
A;Reference number: A93872; MUID:81223722; PMID:7017772
A;Accession: A93872
A;Molecule type: mRNA
A;Residues: 1-608 <SAR>
A;Cross-references: GB:V01222; GB:J00698; NID:955627; PIDN:CAA24532.1; PID:g55628
R;Strauss, A.W.; Bennett, C.D.; Donohue, A.M.; Rodkey, J.A.; Alberts, A.W.
J. Biol. Chem. 252, 6846-6855, 1977
A;Title: Rat liver pre-proalbumin: complete amino acid sequence of the pre-piece. Analysis
A;Reference number: A92211; MUID:77249657; PMID:893447
A;Note: cleavages during protein maturation
A;Accession: A92211
A;Molecule type: protein
A;Residues: 1-38 <STR>
R;Isemura, S.; Ikenaka, T.
J. Biochem. 83, 35-48, 1978
A;Title: Amino acid sequences of fragments I and II obtained by cyanogen bromide cleavage
A;Reference number: A91946; MUID:78109429; PMID:564345
A;Accession: A91946
A;Molecule type: protein
A;Residues: 25-222 <ISI>
R;Isemura, S.; Ikenaka, T.
J. Biochem. 79, 1183-1196, 1976
A;Title: Fragmentation of rat serum albumin by cyanogen bromide cleavage and the amino a
A;Reference number: A91940; MUID:76260153; PMID:956149
A;Accession: A91940
A;Molecule type: protein
A;Residues: 223-288;572-608 <IS2>
A;Note: 262-Leu was also found
R;Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
A;Title: Copper(II)-binding ability of human alpha-fetoprotein.
A;Reference number: A90758; MUID:79001617; PMID:80265
A;Contents: annotation: copper binding
R;Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A;Reference number: A45800; MUID:89341406; PMID:2474609
A;Accession: C45800
A;Status: preliminary
A;Molecule type: protein
A;Residues: 166-173 <CAR>
R;Heard, J.
Mol. Cell. Biol. 7, 2425-2434, 1987
A;Title: Determinants of rat albumin promoter tissue specificity analyzed by an improved
A;Reference number: I57621; MUID:87286876; PMID:3475566
A;Accession: I57621
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M16825; NID:g202828; PIDN:AAA40712.1; PID:g554412
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; plasma
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-608/Product: serum albumin #status experimental <MAT>
F;29-202/Domain: serum albumin repeat homology <SA1>
F;221-394/Domain: serum albumin repeat homology <SA2>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status experimental
F;77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393-4

Query Match 98.3%; Score 57; DB 1; Length 608;
Best Local Similarity 90.9%; Pred. No. 0.006;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||
Db 26 AHKSEVAHRFK 36

RESULT 3
A47391
serum albumin precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
C;Accession: A47391
R;Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam,
Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
A;Title: cDNA and protein sequence of polymorphic macaque albumins that differ in b11
A;Reference number: A47391; MUID:93211971; PMID:8460152
A;Contents: B/B homozygote
A;Accession: A47391
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-609 <MAT>
A;Cross-references: GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:128280, NCBI:128281)
C;Superfamily: serum albumin; serum albumin repeat homology
F;21-194/Domain: serum albumin repeat homology <SA1>
F;213-386/Domain: serum albumin repeat homology <SA2>
F;405-584/Domain: serum albumin repeat homology <SA3>

Query Match 93.1%; Score 54; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRFK 11
|||||
Db 19 HKSEVAHRFK 28

RESULT 4
JC5838
albumin - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 03-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 19-May-2000
C;Accession: JC5838
R;Yoshida, K.; Seto-Ohshima, A.; Sinohara, H.
DNA Res. 4, 351-354, 1997
A;Title: Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in
A;Reference number: JC5838; MUID:98116663; PMID:9455485
A;Accession: JC5838
A;Molecule type: mRNA
A;Residues: 1-609 <YOS>
A;Cross-references: DDBJ:AB006197; NID:g2317277; PIDN:BAA21765.1; PID:g2317278
A;Experimental source: liver
C;Superfamily: serum albumin; serum albumin repeat homology
F;222-395/Domain: serum albumin repeat homology <SA2>

```

Query Match      93.1%; Score 54; DB 2; Length 609;
Best Local Similarity 81.8%; Pred. No. 0.023;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
   |||||:||||:
DB 27 AHKSEIAHRYK 37

RESULT 5
ABBS
serum albumin precursor [validated] - bovine
N:Alternate names: 67K protein; preproalbumin
C:Species: Bos primigenius taurus (Cattle)
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C:Accession: A38885; A36401; A91258; B60808; S10780; D45800; A26693; A90309; A91458; A94
R:Holowachuk, E.W.; Stoltzenberg, J.K.; Reed, R.G.; Peters Jr., T.
submitted to the EMBL Data Library, August 1991
A:Description: Bovine serum albumin: cDNA sequence and expression.
A:Reference number: A38885
A:Accession: A38885
A:Molecule type: mRNA
A:Residues: 1-607 <HOL>
A:Cross-references: EMBL:M73215
R:Hirayana, K.; Akashi, S.; Furuya, M.; Fukuhara, K.
Biochem. Biophys. Res. Commun. 173, 639-646, 1990
A:Title: Rapid confirmation and revision of the primary structure of bovine serum albumin
A:Reference number: A36401; MUID:91083649; PMID:2260975
A:Accession: A36401
A:Molecule type: protein
A:Residues: 25-41,'H',43-189,'E',191-213,'T',215-323,'D',325-393,'TS',396-607 <HIR>
R:Macgillivray, R.T.A.; Chung, D.W.; Davie, E.W.
Eur. J. Biochem. 98, 477-485, 1979
A:Title: Biosynthesis of bovine plasma proteins in a cell-free system.
A:Reference number: A91258; MUID:80024278; PMID:488109
A:Accession: A91258
A:Molecule type: protein
A:Residues: 1-32 <MAG>
R:Hsieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A:Title: Electrophoretic filter from an analytical isoelectrofocusing gel
A:Reference number: A60808; MUID:88267456; PMID:3389500
A:Accession: B60808
A:Molecule type: protein
A:Residues: 25-41 <HSI>
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A:Reference number: S10780; MUID:90336641; PMID:2379503
A:Accession: S10780
A:Molecule type: protein
A:Residues: 25-41,'H',43-57,59-64 <STR>
R:Carraway, R.E.; Cochrane, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A:Title: Structures of histamine-releasing peptides formed by the action of acid proteases
A:Reference number: A45800; MUID:89341406; PMID:2474609
A:Accession: D45800
A:Molecule type: protein
A:Residues: 163-172 <CAR>
R:Carraway, R.E.; Mitra, S.P.; Cochrane, D.E.
J. Biol. Chem. 262, 5968-5973, 1987
A:Title: Structure of a biologically active neurotensin-related peptide obtained from pe
A:Reference number: A26693; MUID:87194805; PMID:2437111
A:Accession: A26693
A:Molecule type: protein
A:Residues: 165-172,'L', <CA2>
R:Reed, R.G.; Putnam, F.W.; Peters Jr., T.
Biochem. J. 191, 867-868, 1980
A:Title: Sequence of residues 400-403 of bovine serum albumin.
A:Reference number: A90309; MUID:82023364; PMID:7283978
A:Accession: A90309
A:Molecule type: protein
A:Residues: 402-433 <REE>
R:Brown, J.R.
Fed. Proc. 34, 591, 1975
A:Title: Structure of bovine serum albumin.
A:Reference number: A91458
A:Accession: A91458
A:Molecule type: protein
A:Residues: 25-41,'H',43-117,'EQ',120-179,181-189,'E',191-194,'A',196-213,'T',215-288
R:Brown, J.R.
submitted to the Atlas, April 1975
A:Reference number: A94551
A:Accession: A94551
A:Molecule type: protein
A:Residues: 190-195 <BR2>
R:Brown, J.R.
Fed. Proc. 33, 1389, 1974
A:Reference number: A91457
A:Contents: annotation; disulfide bonds
R:Werlen, R.C.; Offord, R.E.; Rose, K.
Biochem. J. 302, 907-911, 1994
A:Title: Preparation and characterization of novel substrates of insulin proteinase (
A:Reference number: S55232; MUID:95031935; PMID:7945219
A:Accession: S55232
A:Status: preliminary
A:Molecule type: protein
A:Residues: 529-536;569-572 <WER>
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; copper binding; duplication; plasma
F:1-18/Domain: signal sequence #status experimental <SIG>
F:19-24/Domain: propeptide #status experimental <PRO>
F:25-607/Product: serum albumin #status experimental <MPT>
F:229-201/Domain: serum albumin repeat homology <SA1>
F:220-393/Domain: serum albumin repeat homology <SA2>
F:412-591/Domain: serum albumin repeat homology <SA3>
F:27/Binding site: copper (His) #status predicted
F:77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-393
Query Match      91.4%; Score 53; DB 1; Length 607;
Best Local Similarity 90.0%; Pred. No. 0.035;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRFK 11
   |||||:||||
DB 27 HKSEIAHRYK 36

RESULT 6
ABBS
serum albumin precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: S06936
R:Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
Nucleic Acids Res. 17, 10495, 1989
A:Title: Nucleotide and deduced amino acid sequence of sheep serum albumin.
A:Reference number: S06936; MUID:90098888; PMID:2602160
A:Accession: S06936
A:Molecule type: mRNA
A:Residues: 1-607 <BRO>
A:Cross-references: EMBL:X17055; NID:gl386; PIDN:CA34903.1; PID:gl387
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds coppe
teroid hormones (weak bonds with these hormones promote their transfer across the mem
C:Superfamily: serum albumin; serum albumin repeat homology
C:Keywords: carrier protein; duplication; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: propeptide #status predicted <PRO>
F:25-607/Product: serum albumin #status predicted <MAT>
F:229-201/Domain: serum albumin repeat homology <SA1>
F:220-393/Domain: serum albumin repeat homology <SA2>
F:412-591/Domain: serum albumin repeat homology <SA3>
F:27/Binding site: copper (His) #status predicted
F:77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-393
F:263/Binding site: bilirubin (Lys) #status predicted

```

Query Match 82.8%; Score 48; DB 1; Length 607;
 Best Local Similarity 88.9%; Pred. No. 0.32;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
 |||||
 DB 27 HKSEIAHRF 35

RESULT 7

ABHOS

serum albumin precursor - horse
 C:Species: Equus caballus (domestic horse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: S34053
 R:Ho, J.X.; Holowachuk, E.W.; Norton, E.J.; Twigg, P.D.; Carter, D.C.
 Eur. J. Biochem. 215, 205-212, 1993
 A:Title: X-ray and primary structure of horse serum albumin (Equus caballus) at 0.27-nm
 A:Reference number: S34053; MUID:93345495; PMID:8344282
 A:Accession: S34053
 A:Molecule type: mRNA
 A:Residues: 1-607 <HO>
 A:Cross-references: GB:X74045; NID:G399671; PIDN:CAA52194.1; PID:G399672
 C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, teroid hormones (weak bonds with these hormones promote their transfer across the membrane)
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: carrier protein; duplication; metal binding; plasma
 F:1-18/Domain: signal sequence #status predicted <PRO>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-607/Product: serum albumin #status predicted <MAT>
 F:29-201/Domain: serum albumin repeat homology <SA1>
 F:220-393/Domain: serum albumin repeat homology <SA2>
 F:412-591/Domain: serum albumin repeat homology <SA3>
 F:27/Binding site: copper (His) #status predicted
 F:77-86,99-115,114-125,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,4
 F:263/Binding site: bilirubin (Lys) #status predicted

Query Match 82.8%; Score 48; DB 1; Length 607;
 Best Local Similarity 88.9%; Pred. No. 0.32;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
 |||||
 DB 27 HKSEIAHRF 35

RESULT 8

S57632

serum albumin precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Aug-1999
 C:Accession: JC4660; S57632
 R:Hilger, C.; Grigioni, F.; Hentges, F.
 Gene 169, 295-296, 1996
 A:Title: Sequence of the gene encoding cat (Felis domesticus) serum albumin.
 A:Reference number: JC4660; MUID:96194824; PMID:8647469
 A:Accession: JC4660
 A:Molecule type: mRNA
 A:Residues: 1-608 <HI2>
 A:Cross-references: EMBL:X84842; NID:9886484; PIDN:CAA59279.1; PID:9886485
 A:Experimental source: liver
 C:Comment: This protein is the major protein component in plasma. It functions as a multiein has 35 conserved cysteine residues.
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: liver; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-608/Product: serum albumin #status predicted <MAT>
 F:29-202/Domain: serum albumin repeat homology <SA1>
 F:221-394/Domain: serum albumin repeat homology <SA2>
 F:413-592/Domain: serum albumin repeat homology <SA3>

Query Match 82.8%; Score 48; DB 2; Length 608;

Best Local Similarity 80.0%; Pred. No. 0.32;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 10
 |||||
 DB 26 AHOSEIAHRF 35

RESULT 9

ABPGS

serum albumin precursor - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: S01382; A61006
 R:Weinstock, J.; Baldwin, G.S.
 Nucleic Acids Res. 16, 9045, 1988
 A:Title: Nucleotide sequence of porcine liver albumin.
 A:Reference number: S01382; MUID:89016582; PMID:3174440
 A:Accession: S01382
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-605 <WE1>
 A:Cross-references: EMBL:X12422; NID:91875; PIDN:CAA30970.1; PID:9833798
 R:Limeback, H.; Sakarya, H.; Chu, W.; Mackinnon, M.
 J. Bone Miner. Res. 4, 235-241, 1989
 A:Title: Serum albumin and its acid hydrolysis peptides dominate preparations of mine
 A:Reference number: A61006; MUID:89269769; PMID:2728927
 A:Accession: A61006
 A:Molecule type: protein
 A:Residues: 23-51, 'X', 53-54; 'XXXGY', 146, 'E', 148, 'E', 150-151, 'XVN', 155 <LIM>
 A:Experimental source: dental enamel
 A:Note: albumin and other serum proteins are also found in bone
 C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper teroid hormones (weak bonds with these hormones promote their transfer across the membrane)
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: carrier protein; duplication; metal binding; plasma
 F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>
 F:17-22/Domain: propeptide #status predicted <PRO>
 F:23-605/Product: serum albumin #status predicted <MAT>
 F:27-199/Domain: serum albumin repeat homology <SA1>
 F:218-391/Domain: serum albumin repeat homology <SA2>
 F:410-589/Domain: serum albumin repeat homology <SA3>
 F:75-84,97-113,112-123,145-190,189-198,221-267,266-274,286-300,299-310,337-382,381-39
 F:76/Binding site: bilirubin (Lys) #status predicted

Query Match 81.0%; Score 47; DB 1; Length 605;
 Best Local Similarity 80.0%; Pred. No. 0.49;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 11
 |||||
 DB 25 YKSEIAHRF 34

RESULT 10

ABCHS

serum albumin precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: S15571; A05078; A13451
 R:Cassady, A.I.; Salkild, C.K.; Baverstock, P.; Wallace, J.C.
 submitted to the EMBL Data Library, July 1991
 A:Reference number: S15571
 A:Accession: S15571
 A:Molecule type: mRNA
 A:Residues: 1-615 <CAS>
 A:Cross-references: EMBL:X60688; NID:963747; PIDN:CAA43098.1; PID:963748
 R:Hache, R.J.G.; Wiskocil, R.; Vasa, M.; Roy, R.N.; Lau, P.C.K.; Deeley, R.G.
 J. Biol. Chem. 258, 4556-4564, 1983
 A:Title: The 5' noncoding and flanking regions of the avian very low density apolipop
 A:Reference number: A05078; MUID:83161037; PMID:6187737
 A:Accession: A05078
 A:Molecule type: DNA

A;Residues: 1-28 <HAC>
 A;Cross-references: GB:V00381; NID:g63038; PIDN:CAA23680.1; PID:g63039
 R;Rosen, A.M.; Geller, D.M.
 Biochem. Biophys. Res. Commun. 78, 1060-1066, 1977
 A;Title: Chicken microsomal albumin: amino terminal sequence of chicken proalbumin.
 A;Reference number: A13451; MUID:78019943; PMID:911327
 A;Accession: A13451

A;Molecule type: protein
 A;Residues: 19-23 'M', 25-30 <ROS>
 C;Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, monees (weak bonds with these hormones promote their transfer across the membranes), thyra
 C;Superfamily: serum albumin; serum albumin repeat homology
 C;Keywords: carrier protein; duplication; metal binding; plasma
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-26/Domain: propeptide #status predicted <PRO>
 F:27-613/Product: serum albumin #status predicted <MAT>
 F:22-206/Domain: serum albumin repeat homology <SA1>
 F:325-398/Domain: serum albumin repeat homology <SA2>
 F:417-596/Domain: serum albumin repeat homology <SA3>
 F:30/Binding site: copper (HIS) #status predicted
 F:80-89,102-118,117-128,152-197,196-205,228-274,273-281,293-307,306-317,344-389,388-397,

Query Match 77.6%; Score 45; DB 1; Length 615;
 Best Local Similarity 77.8%; Pred. No. 1.2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
 |||||:||||
 DB 30 HKSEIAHRY 38

RESULT 11

S29749 serum albumin - dog
 C;Species: Canis lupus familiaris (dog)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
 C;Accession: S29749
 R;Dixon, J.W.; Sarkar, B.
 J. Biol. Chem. 249, 5872-5877, 1974
 A;Title: Isolation, amino acid sequence and copper(II)-binding properties of peptide (1-
 A;Reference number: S29749; MUID:75011422; PMID:4414013
 A;Accession: S29749
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <DIX>
 C;Superfamily: serum albumin; serum albumin repeat homology

Query Match 74.1%; Score 43; DB 2; Length 24;
 Best Local Similarity 70.0%; Pred. No. 0.094;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 10
 |::|||:||||
 DB 2 AYKSEIAHRY 11

RESULT 12

B61511 serum albumin, milk-derived - Australian echidna (fragment)
 C;Species: Tachyglossus aculeatus (Australian echidna)
 C;Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
 C;Accession: B61511
 R;Teahan, C.G.; McKenzie, H.A.; Griffiths, M.
 Comp. Biochem. Physiol. B 99, 99-118, 1991
 A;Title: Some monotreme milk "whey" and blood proteins.
 A;Reference number: A61511; MUID:92070088; PMID:1959333
 A;Accession: B61511
 A;Status: preliminary

A;Molecule type: protein
 A;Residues: 1-30 <GRI>
 C;Superfamily: serum albumin; serum albumin repeat homology
 C;Keywords: milk

Query Match 69.0%; Score 40; DB 2; Length 30;
 Best Local Similarity 63.6%; Pred. No. 0.44;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRF 11
 |::|||:||||
 DB 2 AQKSELGHRYK 12

RESULT 13

E82910 hypothetical protein UU287 [imported] - Ureaplasma urealyticum
 C;Species: Ureaplasma urealyticum
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: E82910
 R;Glass, J.I.; Iefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
 A;Reference number: A82870
 A;Accession: E82910
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-201 <GLA>
 A;Cross-references: GB:AE002125; GB:AF222894; NID:g6899253; PIDN:AAF30696.1; GSPDB:GN
 A;Experimental source: serovar 3; biovar 1
 C;Genetics:
 A;Gene: UU287
 A;Genetic code: SGC3

Query Match 68.1%; Score 39.5; DB 2; Length 201;
 Best Local Similarity 52.6%; Pred. No. 4.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 2 HKS-----EVAHRFK 11
 |||||
 DB 79 HKSSSLYLTNDDEVAHRFK 97

RESULT 14

AH2378 hypothetical protein asr4584 [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AH2378
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AH2378
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-93 <KUR>
 A;Cross-references: GB:BA000019; PIDN:BA076283.1; PID:g17133720; GSPDB:GN00179
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: asr4584

Query Match 63.8%; Score 37; DB 2; Length 93;
 Best Local Similarity 66.7%; Pred. No. 5.5;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HKSEVAHRF 10
 |::|||:||||
 DB 46 HAADVVAHRF 54

RESULT 15

T30740 hypothetical protein 138R - Molluscum contagiosum virus 1
 N;Alternate names: MC138R
 C;Species: Molluscum contagiosum virus 1

C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C:Accession: T30740
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A>Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A:Reference number: Z20876; MUID:96325459; PMID:8670425
A:Accession: T30740
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-117 <SEN>
A:Cross-references: EMBL:U60315; PIDN:AAC55266.1
C:Genetics:
A:Note: MC138R
C:Superfamily: variola major virus 6R protein

Query Match	62.1%	Score 36;	DB 2;	Length 117;
Best Local Similarity	77.8%	Pred. No. 11;		
Matches	7;	Conservative	0;	Mismatches 2;
		Indels	0;	Gaps 0;
QY	1	AHKSEVAHR	9	
DB	24	AHKSFAHR	32	

Search completed: August 29, 2003, 14:29:28
Job time : 40 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 29, 2003, 14:27:05 ; Search time 24 Seconds
(without alignments)
13.562 Million cell updates/sec

Title: US-09-845-726A-1_COPY_2_12

Perfect score: 58

Sequence: 1 AHKSEVAHRFK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141812 seqs, 29589763 residues

Total number of hits satisfying chosen parameters: 141812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA.New.*
1: /cgn2.6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2.6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2.6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2.6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2.6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2.6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2.6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	54	6 US-10-273-573-10524	Sequence 10524, A
2	58	100.0	76	6 US-10-273-573-5999	Sequence 5999, Ap
3	58	100.0	133	6 US-10-273-573-5979	Sequence 5979, Ap
4	58	100.0	134	6 US-10-273-573-5922	Sequence 5922, Ap
5	58	100.0	156	6 US-10-273-573-5921	Sequence 5921, Ap
6	58	100.0	192	6 US-10-273-573-5924	Sequence 5924, Ap
7	58	100.0	214	6 US-10-273-573-5923	Sequence 5923, Ap
8	58	100.0	289	6 US-10-273-573-5569	Sequence 5569, Ap
9	58	100.0	401	6 US-10-273-573-5925	Sequence 5925, Ap
10	58	100.0	520	6 US-10-273-573-5926	Sequence 5926, Ap
11	58	100.0	550	6 US-10-273-573-5927	Sequence 5927, Ap
12	58	100.0	585	1 PCT-US03-18896-26	Sequence 26, Appl
13	58	100.0	585	1 PCT-US03-19902-3	Sequence 3, Appl
14	58	100.0	585	6 US-10-462-262-26	Sequence 26, Appl
15	58	100.0	585	6 US-10-602-141-3	Sequence 3, Appl
16	58	100.0	585	6 US-10-424-999-11	Sequence 11, Appl
17	58	100.0	585	6 US-10-425-000-31	Sequence 31, Appl
18	58	100.0	604	6 US-10-408-765A-55	Sequence 55, Appl
19	58	100.0	609	6 US-10-408-765A-2	Sequence 2, Appl
20	58	100.0	609	6 US-10-609-346-12	Sequence 12, Appl
21	58	100.0	609	7 US-60-490-890-752	Sequence 752, App
22	58	100.0	609	7 US-60-490-419-1	Sequence 1, Appl
23	58	100.0	609	7 US-60-490-149-1	Sequence 1, Appl
24	58	100.0	672	6 US-10-424-999-15	Sequence 15, Appl
25	58	100.0	672	6 US-10-425-000-35	Sequence 35, Appl
26	58	100.0	674	6 US-10-424-999-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-10-273-573-10524
; Sequence 10524, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 10524
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-573-10524

Query Match:

Best Local Similarity 100.0%; Score 58; DB 6; Length 54;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AHKSEVAHRFK 11

Db 21 AHKSEVAHRFK 31

RESULT 2

US-10-273-573-5999
; Sequence 5999, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5999
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens

Sequence 34, Appl
Sequence 10514, A
Sequence 17, Appl
Sequence 37, Appl
Sequence 18, Appl
Sequence 38, Appl
Sequence 13, Appl
Sequence 33, Appl
Sequence 10, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 5928, Ap
Sequence 5931, Ap
Sequence 8, Appl
Sequence 2, Appl
Sequence 6000, Ap
Sequence 5930, Ap
Sequence 5929, Ap
Sequence 5708, Ap

674 6 US-10-425-000-34
684 6 US-10-273-573-10514
687 6 US-10-424-999-17
687 6 US-10-425-000-37
688 6 US-10-424-999-18
688 6 US-10-425-000-38
689 6 US-10-424-999-13
689 6 US-10-425-000-33
712 6 US-10-609-346-10
712 6 US-10-609-346-4
746 6 US-10-609-346-6
750 6 US-10-273-573-5928
750 6 US-10-273-573-5931
759 6 US-10-609-346-8
763 6 US-10-609-346-2
787 6 US-10-273-573-6000
789 6 US-10-273-573-5930
879 6 US-10-273-573-5929
978 6 US-10-273-573-5708

US-10-273-573-5999

Query Match 100.0%; Score 58; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||
Db 37 AHKSEVAHRFK 47

RESULT 3

US-10-273-573-5979
; Sequence 5979, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5979
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)..(127)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by EMATRIX,
; OTHER INFORMATION: accession number PR00802A, p-value=2.324e-14, raw score of 12.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (30)..(132)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=2.8e-10, PFam score of 47.6
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(133)
; OTHER INFORMATION: Xaa = x or * as defined in Table 2

US-10-273-573-5979

Query Match 100.0%; Score 58; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||
Db 28 AHKSEVAHRFK 38

RESULT 4

US-10-273-573-5922
; Sequence 5922, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5922
; LENGTH: 134
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (58)..(134)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=0.00037, PFam score of -21.7
US-10-273-573-5922

Query Match 100.0%; Score 58; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||
Db 56 AHKSEVAHRFK 66

RESULT 5

US-10-273-573-5921
; Sequence 5921, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5921
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (120)..(135)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by EMATRIX,
; OTHER INFORMATION: accession number PR00802A, p-value=1.000e-19, raw score of 12.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (35)..(153)
; OTHER INFORMATION: Serum albumin family domain identified by PFam, accession
; OTHER INFORMATION: name transport_prot, E-value=3.7e-26, PFam score of 100.3
US-10-273-573-5921

Query Match 100.0%; Score 58; DB 6; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||
Db 33 AHKSEVAHRFK 43

RESULT 6

US-10-273-573-5924
; Sequence 5924, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5924

```

; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (130)..(154)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; accession number PR00802B, p-value=6.294e-24, raw score of 16.51
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (56)..(185)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; number PR00802A, p-value=3.066e-09, raw score of 12.
; OTHER INFORMATION: name transport_prot, E-value=6.6e-26, Pfam score of 99.5
US-10-273-573-5924

```

```

Query Match 100.0%; Score 58; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AHKSEVAHRFK 11
Db 54 AHKSEVAHRFK 64

```

RESULT 7

```

US-10-273-573-5923
; Sequence 5923, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5923
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (149)..(173)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; accession number PR00802B, p-value=6.294e-24, raw score of 16.51
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (40)..(204)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; number PR00802A, p-value=3.066e-09, raw score of 12.
US-10-273-573-5923

```

```

Query Match 100.0%; Score 58; DB 6; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AHKSEVAHRFK 11
Db 38 AHKSEVAHRFK 48

```

RESULT 8

```

US-10-273-573-5569
; Sequence 5569, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18

```

```

; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5569
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (125)..(140)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; accession number PR00802A, p-value=3.066e-09, raw score of 12.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (41)..(230)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; number PR00802A, p-value=3.066e-09, raw score of 12.
; OTHER INFORMATION: name transport_prot, E-value=6.6e-26, Pfam score of 99.5
; NAME/KEY: misc feature
; LOCATION: (1)..(289)
; OTHER INFORMATION: Xaa - X or * as defined in Table 2
US-10-273-573-5569

```

```

Query Match 100.0%; Score 58; DB 6; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AHKSEVAHRFK 11
Db 38 AHKSEVAHRFK 48

```

RESULT 9

```

US-10-273-573-5925
; Sequence 5925, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5925
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (161)..(185)
; OTHER INFORMATION: SERUM ALBUMIN FAMILY SIGNATURE domain identified by eMATRIX,
; accession number PR00802B, p-value=6.294e-24, raw score of 16.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (41)..(384)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; number PR00802A, p-value=3.066e-09, raw score of 12.
US-10-273-573-5925

```

```

Query Match 100.0%; Score 58; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 AHKSEVAHRFK 11
Db 39 AHKSEVAHRFK 49

```

```

RESULT 10
US-10-273-573-5926
; Sequence 5926, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5926
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (158)..(210)
; OTHER INFORMATION: Serum albumin family proteins domain identified by eMATRIX,
; accession number BL00212, p-value=1.000e-40, raw score of 30.19
US-10-273-573-5926
; NAME/KEY: DOMAIN
; LOCATION: (44)..(503)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; number transport_prot, E-value=2.6e-126, Pfam score of 433.1
US-10-273-573-5926

Query Match      100.0%; Score 58; DB 6; Length 520;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
DB      42 AHKSEVAHRFK 52
|||||

RESULT 11
US-10-273-573-5927
; Sequence 5927, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5927
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (188)..(240)
; OTHER INFORMATION: Serum albumin family proteins domain identified by eMATRIX,
; accession number BL00212, p-value=1.000e-40, raw score of 30.19
US-10-273-573-5927
; NAME/KEY: DOMAIN
; LOCATION: (30)..(534)
; OTHER INFORMATION: Serum albumin family domain identified by Pfam, accession
; number transport_prot, E-value=1.2e-150, Pfam score of 513.9
US-10-273-573-5927

```

```

Query Match      100.0%; Score 58; DB 6; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
DB      28 AHKSEVAHRFK 38
|||||

RESULT 12
PCT-US03-18896-26
; Sequence 26, Application PC/TUS0318896
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052W01
; CURRENT APPLICATION NUMBER: PCT/US03/18896
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US03-18896-26

Query Match      100.0%; Score 58; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
DB      2 AHKSEVAHRFK 12
|||||

RESULT 13
PCT-US03-19902-3
; Sequence 3, Application PC/TUS0319902
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: SERUM PROTEIN-ASSOCIATED TARGET-SPECIFIC
; LIGANDS AND IDENTIFICATION METHOD THEREFOR
; FILE REFERENCE: 10280-058W01
; CURRENT APPLICATION NUMBER: PCT/US03/19902
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/390,657
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US03-19902-3

Query Match      100.0%; Score 58; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AHKSEVAHRFK 11
DB      2 AHKSEVAHRFK 12
|||||

RESULT 14
US-10-462-262-26
; Sequence 26, Application US/10462262
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS

```

```
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-262-26
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; Sequence 3, Application US/10602141
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; TITLE OF INVENTION: SERUM PROTEIN-ASSOCIATED TARGET-SPECIFIC
; TITLE OF INVENTION: LIGANDS AND IDENTIFICATION METHOD THEREFOR
; FILE REFERENCE: 10280-058001
; CURRENT APPLICATION NUMBER: US/10/602,141
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 60/390,657
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-602-141-3
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Best Local Similarity 100.0%; Pred. No. 0.0012;
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Job time : 25 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: August 29, 2003, 14:26:35 ; Search time 378 Seconds
(without alignments)
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Perfect score: 58

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SUMMARIES

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2	58	100.0	11 1	PCT-US02-04275-4

3	58	100.0	11	PCT-US02-37136-4
4	58	100.0	11	US-09-678-202A-4
5	58	100.0	11	US-09-845-726-1
6	58	100.0	11	US-10-076-071-4
7	58	100.0	11	US-10-186-168-4
8	58	100.0	11	US-10-300-664-4
9	58	100.0	12	PCT-US00-26952-3
10	58	100.0	12	PCT-US00-26952-6
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19	58	100.0	12	US-10-076-071-6
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21	58	100.0	12	US-10-186-168-6
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25	58	100.0	13	US-09-266-768-13
26	58	100.0	13	US-09-845-726A-1
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28	58	100.0	15	US-09-845-764A-1
29	58	100.0	17	US-09-845-727-1
30	58	100.0	20	US-08-840-752A-4
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ALIGNMENTS

RESULT 1

PCT-US00-26952-4
; Sequence 4, Application PC/TUS0026952
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/26952
; CURRENT FILING DATE: 2000-09-30
; EARLIER APPLICATION NUMBER: 60/157,404
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 60/211,078
; EARLIER FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-26952-4

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Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AHKSEVAHRFK 11

RESULT 2

PCT-US02-04275-4
; Sequence 4, Application PC/TUS0204275
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/04275
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-04275-4

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RESULT 3

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; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ORAL CARE
; FILE REFERENCE: 4172-75-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/37136
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

PCT-US02-37136-4

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US-09-678-202A-4
; Sequence 4, Application US/09678202A
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/09/678,202A
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-678-202A-4

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; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; TITLE OF INVENTION: OF 1424 DALTONS
; FILE REFERENCE: 2132.033
; CURRENT APPLICATION NUMBER: US/09/845,726
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-726-1

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; Sequence 4, Application US/10076071
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2
; CURRENT APPLICATION NUMBER: US/10/076,071
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
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; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-071-4

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; Sequence 4, Application US/10186168
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
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; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
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; SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-168-4

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; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/300,664
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/678,202
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; PRIOR FILING DATE: 1999-10-01
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Db 1 AHKSEVAHRFK 11

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; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3-PCT
; CURRENT APPLICATION NUMBER: PCT/US00/26952
; CURRENT FILING DATE: 2000-09-30
; EARLIER APPLICATION NUMBER: 60/157,404
; EARLIER FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: 60/211,078
; EARLIER FILING DATE: 2000-06-13
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; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-26952-3

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; Sequence 3, Application PC/TUS0237136
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David

; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ORAL CARE
; FILE REFERENCE: 4172-75-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/37136
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
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; ORGANISM: Homo sapiens
PCT-US02-37136-3

Query Match 100.0%; Score 58; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AHKSEVAHRFK 12

RESULT 14

PCT-US02-37136-6
; Sequence 6, Application PC/TUS0237136
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ORAL CARE
; FILE REFERENCE: 4172-75-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/37136
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
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; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
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Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AHKSEVAHRFK 12

RESULT 15

US-09-678-202A-3
; Sequence 3, Application US/09678202A
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/09/678, 202A
; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-678-202A-3

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Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AHKSEVAHRFK 12

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Job time : 439 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 14:28:50 ; Search time 56 Seconds
(without alignments)
26.868 Million cell updates/sec

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Perfect score: 58
Sequence: 1 AHKSEVAHRFK 11

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	10	US-09-845-726-1
2	58	100.0	11	12	US-10-300-664-4
3	58	100.0	11	15	US-10-076-071-4
4	58	100.0	11	16	US-10-186-168-4
5	58	100.0	12	11	US-09-846-347-1
6	58	100.0	12	12	US-10-300-664-3
7	58	100.0	12	12	US-10-300-664-6
8	58	100.0	12	15	US-10-076-071-3
9	58	100.0	12	15	US-10-076-071-6
10	58	100.0	12	16	US-10-186-168-3
11	58	100.0	12	16	US-10-186-168-6
12	58	100.0	13	10	US-09-845-764-1
13	58	100.0	17	10	US-09-845-727-1
14	58	100.0	24	10	US-09-846-328-1
15	58	100.0	26	10	US-09-846-329-1

16	58	100.0	195	14	US-10-074-956-24	Sequence 24, Appl
17	58	100.0	241	14	US-10-074-956-27	Sequence 27, Appl
18	58	100.0	268	14	US-10-074-956-28	Sequence 28, Appl
19	58	100.0	585	11	US-09-929-552-2	Sequence 2, Appl
20	58	100.0	585	11	US-09-932-613-445	Sequence 445, Appl
21	58	100.0	585	11	US-09-984-010-26	Sequence 26, Appl
22	58	100.0	585	11	US-09-833-041-18	Sequence 18, Appl
23	58	100.0	585	12	US-10-153-604A-5	Sequence 5, Appl
24	58	100.0	585	14	US-10-153-064-5	Sequence 5, Appl
25	58	100.0	604	11	US-09-984-010-7	Sequence 7, Appl
26	58	100.0	609	11	US-09-919-039-370	Sequence 370, Appl
27	58	100.0	609	12	US-10-153-604A-7	Sequence 7, Appl
28	58	100.0	609	14	US-10-153-064-7	Sequence 7, Appl
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30	58	100.0	610	15	US-10-237-667-2	Sequence 2, Appl
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32	58	100.0	610	15	US-10-237-866-2	Sequence 2, Appl
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34	58	100.0	610	15	US-10-237-624-2	Sequence 2, Appl
35	58	100.0	651	12	US-10-153-604A-133	Sequence 133, App
36	58	100.0	651	14	US-10-153-064-133	Sequence 133, App
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38	58	100.0	652	12	US-10-153-604A-99	Sequence 99, Appl
39	58	100.0	652	12	US-10-153-604A-105	Sequence 105, App
40	58	100.0	652	12	US-10-153-604A-132	Sequence 132, App
41	58	100.0	652	14	US-10-153-064-96	Sequence 96, Appl
42	58	100.0	652	14	US-10-153-064-99	Sequence 99, Appl
43	58	100.0	652	14	US-10-153-064-105	Sequence 105, App
44	58	100.0	652	14	US-10-153-064-132	Sequence 132, App
45	58	100.0	653	12	US-10-153-604A-131	Sequence 131, App

ALIGNMENTS

RESULT 1
US-09-845-726-1
; Sequence 1, Application US/09845726
; Patent No. US20020160417A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132, 033
; CURRENT APPLICATION NUMBER: US/09/845,726
; CURRENT FILING DATE: 2000-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-726-1

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Matches 11; /Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AHKSEVAHRFK 11

RESULT 2
US-10-300-664-4
; Sequence 4, Application US/10300664
; Publication No. US2003015811A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.

; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/300,664
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-664-4

Query Match 100.0%; Score 58; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
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Db 1 AHKSEVAHREFK 11

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US-10-076-071-4
; Sequence 4, Application US/10076071
; Publication No. US20030060408A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2
; CURRENT APPLICATION NUMBER: US/10/076,071
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-071-4

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-186-168-4
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; Publication No. US20030130185A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-168-4

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Db 1 AHKSEVAHREFK 11

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; Publication No. US20030040602A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132,032
; CURRENT APPLICATION NUMBER: US/09/846,347
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-347-1

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Db 2 AHKSEVAHREFK 12

RESULT 6
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; Sequence 3, Application US/10300664
; Publication No. US2003015811A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David

APPLICANT: Curtis, C. G.
APPLICANT: Lau, Edward
APPLICANT: Rao, Nagaraja K.R.
APPLICANT: Winkler, James V.
APPLICANT: Crook, Wannell M.
TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
FILE REFERENCE: 4172-3
CURRENT APPLICATION NUMBER: US/10/300,664
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US/09/678,202
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2000-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-10-300-664-3

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QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
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US-10-300-664-6
Sequence 6, Application US/10300664
Publication No. US20030158111A1
GENERAL INFORMATION:
APPLICANT: Bar-Or, David
APPLICANT: Curtis, C. G.
APPLICANT: Lau, Edward
APPLICANT: Rao, Nagaraja K.R.
APPLICANT: Winkler, James V.
APPLICANT: Crook, Wannell M.
TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
FILE REFERENCE: 4172-3
CURRENT APPLICATION NUMBER: US/10/300,664
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US/09/678,202
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2000-06-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
US-10-300-664-6

Query Match 100.0%; Score 58; DB 12; Length 12;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AHKSEVAHRFK 12
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RESULT 8
US-10-076-071-3
Sequence 3, Application US/10076071
Publication No. US20030060408A1
GENERAL INFORMATION:
APPLICANT: Bar-Or, David
APPLICANT: Curtis, C. Gerald
APPLICANT: Lau, Edward
APPLICANT: Rao, Nagaraja K.R.
APPLICANT: Winkler, James V.
APPLICANT: Crook, Wannell M.
TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
FILE REFERENCE: 4172-3-2
CURRENT APPLICATION NUMBER: US/10/076,071
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/678,202
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/283,507
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/816,679
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: 60/268,558
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-10-076-071-3

Query Match 100.0%; Score 58; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AHKSEVAHRFK 12
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RESULT 9
US-10-076-071-6
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Publication No. US20030060408A1
GENERAL INFORMATION:
APPLICANT: Bar-Or, David
APPLICANT: Curtis, C. Gerald
APPLICANT: Lau, Edward
APPLICANT: Rao, Nagaraja K.R.
APPLICANT: Winkler, James V.
APPLICANT: Crook, Wannell M.
TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
FILE REFERENCE: 4172-3-2
CURRENT APPLICATION NUMBER: US/10/076,071
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: 09/678,202
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/283,507
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/816,679
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/157,404
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2001-02-13

; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
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; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
US-10-076-071-6

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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; Publication No. US20030130185A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-186-168-3

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Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AHKSEVAHRFK 12
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RESULT 11
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; Publication No. US20030130185A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.

; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
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; SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLATION
US-10-186-168-6

Query Match 100.0%; Score 58; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AHKSEVAHRFK 12
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RESULT 12

US-09-845-764-1
; Sequence 1, Application US/09845764
; Patent No. US20020160958A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132.037
; CURRENT APPLICATION NUMBER: US/09/845,764
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
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; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-764-1

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Qy 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12
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RESULT 13

US-09-845-727-1
; Sequence 1, Application US/09845727
; Patent No. US20020160418A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECUL
; FILE REFERENCE: 2132.047
; CURRENT APPLICATION NUMBER: US/09/845,727
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

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; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-727-1

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Best Local Similarity 100.0%; Pred. No. 0.00038;
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Db      2 AHKSEVAHREK 12
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US-09-846-328-1
; Sequence 1, Application US/09846328
; Patent No. US20020160531A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.051
; CURRENT APPLICATION NUMBER: US/09/846,328
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-328-1

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Db      2 AHKSEVAHREK 12
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RESULT 15
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; Sequence 1, Application US/09846329
; Patent No. US20020161177A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having A Molecular
; FILE REFERENCE: 2132.052
; CURRENT APPLICATION NUMBER: US/09/846,329
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-329-1

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Db      2 AHKSEVAHREK 12
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	13	2	US-08-803-364-7
2	58	100.0	13	2	US-09-024-198-13
3	58	100.0	13	2	US-09-186-409-13
4	58	100.0	585	1	US-08-153-799-14
5	58	100.0	585	1	US-08-448-196A-3
6	58	100.0	585	2	US-08-984-176-1
7	58	100.0	585	2	US-08-702-572-2
8	58	100.0	585	3	US-08-769-746-2
9	58	100.0	609	1	US-08-222-619-3
10	58	100.0	609	1	US-08-433-037-4
11	58	100.0	609	4	US-08-897-956A-2
12	58	100.0	609	5	PCT-US95-04075-3
13	58	100.0	610	2	US-08-797-689-2
14	58	100.0	783	1	US-08-256-938-2
15	58	100.0	787	1	US-08-256-938-4
16	58	100.0	787	2	US-08-797-689-16
17	58	100.0	978	4	US-08-897-956A-3
18	57	98.3	584	1	US-08-448-196A-7
19	53	91.4	582	1	US-08-134-638-1
20	53	91.4	583	1	US-08-448-196A-4
21	50	86.2	13	2	US-08-803-364-6
22	50	86.2	13	2	US-09-024-198-12
23	50	86.2	13	2	US-09-186-409-12
24	50	86.2	16	2	US-08-803-364-1
25	50	86.2	16	2	US-09-024-198-10
26	50	86.2	16	2	US-09-186-409-10
27	48	82.8	583	1	US-08-448-196A-5

Sequence 6, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 5307, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4377, Ap
Sequence 28283, A
Sequence 27825, A
Sequence 28, Appl
Sequence 73, Appl
Sequence 11, Appl
Sequence 196, App

ALIGNMENTS

RESULT 1
US-08-803-364-7
; Sequence 7, Application US/08803364
; Patent No. 5864014
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,364
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/_____
; FILING DATE: 20 FEB 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-6888
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
US-08-803-364-7

Query Match 100.0%; Score 58; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
|||||||

— — —

REFERENCE/DOCKET NUMBER: XX/MFS-28402-2

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/702.572
;; FILING DATE: 11-NOV-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO 95/23857
;; FILING DATE: 1-MAR-1995
;; APPLICATION NUMBER: GB 9404270.2
;; FILING DATE: 5-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Naomi Biswas
;; REGISTRATION NUMBER: 38,384
;; REFERENCE/DOCKET NUMBER: C60114 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610/878/4294
;; TELEFAX: 610/878/4221
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 585 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-702-572-2

Query Match 100.0%; Score 58; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12

RESULT 8
US-08-769-746-2
;; Sequence 2, Application US/08769746
;; Patent No. 6274305
;; GENERAL INFORMATION:
;; APPLICANT: Sonnenschein, Carlos
;; APPLICANT: Soto, Ana M.
;; TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
;; NUMBER OF SEQUENCES: 2
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Medlen & Carroll, LLP
;; STREET: 220 Montgomery Street, Suite 2200
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/769,746
;; FILING DATE: 19-DEC-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Carroll, Peter G.
;; REGISTRATION NUMBER: 32,837
;; REFERENCE/DOCKET NUMBER: MBRI-02584
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 585 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-769-746-2

Query Match 100.0%; Score 58; DB 3; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12

RESULT 9
US-08-222-619-3
;; Sequence 3, Application US/08222619
;; Patent No. 5652352
;; GENERAL INFORMATION:
;; APPLICANT: Lichenstein, Henri
;; APPLICANT: Lyons, David
;; APPLICANT: Wurfel, Mark
;; APPLICANT: Wright, Samuel
;; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
;; TITLE OF INVENTION: Protein
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Center, Patent Operations/RRC
;; STREET: 1840 DeHavilland Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: U.S.
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/222,619
;; FILING DATE:
;; CLASSIFICATION: 435
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 609 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-222-619-3

Query Match 100.0%; Score 58; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 26 AHKSEVAHRFK 36

RESULT 10
US-08-433-037-4
;; Sequence 4, Application US/08433037
;; Patent No. 5707828
;; GENERAL INFORMATION:
;; APPLICANT: Sreekrishna, Kotikanyadan
;; APPLICANT: Barr, Kathryn A.
;; APPLICANT: Brerley, Russell A.
;; APPLICANT: Thill, Gregory P.
;; APPLICANT: Tschopp, Juerg F.
;; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
;; TITLE OF INVENTION: PICHIA PASTORIS
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Scully, Scott, Murphy & Presser
;; STREET: 400 Garden City Plaza
;; CITY: Garden City
;; STATE: New York

; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,037
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 91082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US-897-956A-2

Query Match 100.0%; Score 58; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
DB 26 AHKSEVAHRFK 36

RESULT 11
US-08-897-956A-2
; Sequence 2, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-08-897-956A-2

Query Match 100.0%; Score 58; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
DB 26 AHKSEVAHRFK 36

RESULT 12
PCT-US95-04075-3
; Sequence 3, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like

; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US95-04075-3

Query Match 100.0%; Score 58; DB 5; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
| | | | | | | | | |
DB 26 AHKSEVAHRFK 36

RESULT 13
US-08-797-689-2
; Sequence 2, Application US/08797689
; Patent No. 5876969
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guitton, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085

; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38 619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-797-689-2

Query Match 100.0%; Score 58; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
Db 26 AHKSEVAHREFK 36

RESULT 14
US-08-256-938-2
; Sequence 2, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 783 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-256-938-2

Query Match 100.0%; Score 58; DB 1; Length 783;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
Db 26 AHKSEVAHREFK 36

RESULT 15
US-08-256-938-4
; Sequence 4, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; TITLE OF INVENTION: COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3043
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-256-938-4

Query Match 100.0%; Score 58; DB 1; Length 787;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHREFK 11
Db 204 AHKSEVAHREFK 214

Search completed: August 29, 2003, 14:30:04
Job time : 30 secs

✓ 10202

OS	Synthetic.	
XX		
PN	WO200125265-A1.	
XX		
PD	12-APR-2001.	
XX		
PF	29-SEP-2000; 2000WO-US26952.	
XX		
PR	01-OCT-1999; 98US-0157404.	
PR	13-JUN-2000; 2000US-0211078.	
XX		
PA	(BARO/) BAR-OR D.	
PA	(CURT/) CURTIS C G.	
PA	(LAUE/) LAU E.	
PA	(RAON/) RAO N K R.	
PA	(WINK/) WINKLER J V.	
PA	(CROO/) CROOK W M.	
PI	Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;	

XX DR WPI; 2001-328322/34.

XX PT Metal binding peptide compounds prevent damage by reactive oxygen

XX PT species in animal organs and tissues, useful for reperfusion,

XX PT transplantation and treating e.g. ischemia, neurological and

XX PT cardiovascular diseases

XX Example 10; Page 43; 124pp; English.

XX CC The present invention relates to metal binding peptides that prevent

XX CC damage by reactive oxygen. The peptides may be used for reperfusion

XX CC an ischemic tissue or organ with cerebral or cardiovascular ischemia,

XX CC for treating neurological trauma and for neurodegenerative disease.

XX CC The present sequence is a reactive oxygen species inhibitory peptide.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 58; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11

DB 1 AHKSEVAHRFK 11

RESULT 2

AAE14802

ID AAE14802 standard; peptide; 11 AA.

AC AAE14802;

DT 24-FEB-2003 (first entry)

DE Human reactive oxygen species generation inhibiting peptide #2.

XX KW Reactive oxygen species; ROS; metal-binding peptide; angiogenesis;

XX KW embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;

XX KW connective tissue disease; ocular angiogenic disease; polyposis;

XX KW cardiovascular disease; cerebral vascular disease; immune disorder;

XX KW sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;

XX KW cancer; cystic fibrosis; diabetes; hepatitis C; infertility;

XX KW inflammation; inflammatory bowel disease; neurological disease;

XX KW multiple sclerosis; pancreatitis; human.

XX OS Homo sapiens.

XX PN WO200264620-A2.

XX PD 22-AUG-2002.

XX PF 13-FEB-2002; 2002WO-US04275.

XX PR 13-FEB-2001; 2001US-268558P.

XX PR 22-MAR-2001; 2001US-0816679.

XX PR 04-APR-2001; 2001US-281648P.

XX PR 11-APR-2001; 2001US-283507P.

XX PA (DMTB-) DMI BIOSCIENCES INC.

XX PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;

XX PI WPI; 2002-691590/74.

XX PT New method for the inhibition of angiogenesis and the treatment of

XX PT angiogenic disease, sepsis, and a disease involving acidosis, comprises

XX PT the administration of a specified peptide or its salt -

XX PS Example 10; Page 56; 129pp; English.

XX CC The invention relates to a method for reducing molecular, cellular

XX CC and tissue damage done by reactive oxygen species (ROS) and also

XX CC reducing concentration of a metal ion in an animal using specific

XX CC metal-binding peptides and their derivatives that bind metal ions.

XX CC The compounds of the invention are useful for inhibiting angiogenesis

XX CC (including required for embryo implantation e.g. in endometriosis), and

XX CC for treating angiogenic diseases, such as tumour (preferably a benign

XX CC tumour), tumour metastasis, hypertrophy, connective tissue disorder,

XX CC psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral

XX CC vascular disease, polyposis, obesity, immune disorder, sepsis, and a

XX CC disease or condition involving acidosis. The compounds are also useful in

XX CC the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension,

XX CC senility and impotence), arthritis, asthma, autoimmune diseases,

XX CC cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's

XX CC disease, cystic fibrosis, (neuro)degenerative diseases, diabetes

XX CC (diabetic retinopathy, renal disease, impotence and peripheral vascular

XX CC disease), eye diseases, emphysema, head and traumatic brain injury,

XX CC hepatitis C, infertility, inflammation, inflammatory bowel disease,

XX CC metastasis, ischaemia, neoplastic diseases, neurological diseases,

XX CC multiple sclerosis, pancreatitis, peripheral vascular disease, prion

XX CC disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock,

XX CC tissue damage, toxic reactions (e.g. poisoning (herbicide, transition

XX CC metal, carbon monoxide, and antibiotic toxicity). The present

XX CC sequence is a human peptide that inhibits generation of reactive

XX CC oxygen species (ROS).

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 58; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.2e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11

DB 1 AHKSEVAHRFK 11

RESULT 3

ABG75656

ID ABG75656 standard; Peptide; 11 AA.

AC ABG75656;

DT 13-MAY-2003 (first entry)

DE Congestive heart failure disease specific marker #1.

XX KW Biopolymer marker; serum albumin; disease specific marker;

XX KW congestive heart failure.

XX OS Unidentified.

XX PN US2002160417-A1.

XX PD 31-OCT-2002.

XX PF 30-APR-2001; 2001US-0845726.

XX PR 30-APR-2001; 2001US-0845726.

XX PA (JACK/) JACKOWSKI G.

XX PA (STAN/) STANTON EB.

XX PA (THAT/) THATCHER B.

XX PA (VREE/) VREES T.

XX PA (YANT/) YANTHA J.

XX PA (MARS/) MARSHALL J.

XX PI Jackowski G, Stanton EB, Thatcher B, Vrees T, Yantha J;

XX PI Marshall J;

XX DR WPI; 2003-246641/25.

XX PT Novel biopolymer marker such as serum albumin having specific molecular

XX PT weight, useful in indicating disease state such as congestive heart

XX PT failure

XX
PS Claim 1; Page 7; 10pp; English.
CC The invention relates to a biopolymer marker such as serum albumin having
CC a molecular weight of about 1424 daltons, useful in indicating at least
CC one particular disease state. The biopolymer marker is useful for
CC indicating at least one particular disease state such as congestive heart
CC failure and as an antigen in immunoassays for the detection of those
CC individuals suffering from the disease known to be evidenced by the
CC marker sequence. The biopolymer marker rapidly and accurately diagnoses a
CC disease state such as congestive heart failure and allows physicians to
CC identify asymptomatic patients before they develop the disease state.
CC This sequence represents a congestive heart failure disease specific
CC marker.

XX SQ Sequence 11 AA;
Query Match 100.0%; Score 58; DB 24; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 1 AHKSEVAHRFK 11

RESULT 4
AAB74367
ID AAB74367 standard; peptide; 12 AA.

XX AC AAB74367;
XX DT 02-JUL-2001 (first entry)
XX DE Reactive oxygen species inhibitory peptide #3.
XX KW ROS; reactive oxygen species; metal binding; ischemia;
XX KW neurodegenerative.
XX OS Synthetic.
XX PN WO200125265-A1.
XX PD 12-APR-2001.
XX PF 29-SEP-2000; 2000WO-US26952.
XX PR 01-OCT-1999; 99US-0157404.
XX PR 13-JUN-2000; 2000US-0211078.

XX PA (BARO/) BAR-OR D.
XX PA (CURT/) CURTIS C G.
XX PA (LAUE/) LAU E.
XX PA (RAON/) RAO N K R.
XX PA (WINK/) WINKLER J V.
XX PA (CROO/) CROOK W M.
XX PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
XX WPI; 2001-328322/34.
XX PT Metal binding peptide compounds prevent damage by reactive oxygen
XX PT species in animal organs and tissues, useful for reperfusion,
XX PT transplantation and treating e.g. ischemia, neurological and
XX PT cardiovascular diseases -
XX PS Example 10; Page 43; 124pp; English.
XX CC The present invention relates to metal binding peptides that prevent
XX CC damage by reactive oxygen. The peptides may be used for reperfusion,
XX CC an ischemic tissue or organ with cerebral or cardiovascular ischemia,
XX CC for treating neurological trauma and for neurodegenerative disease.
XX CC The present sequence is a reactive oxygen species inhibitory peptide.

XX SQ Sequence 12 AA;
Query Match 100.0%; Score 58; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12

RESULT 5
AAB74370
ID AAB74370 standard; peptide; 12 AA.

XX AC AAB74370;
XX DT 02-JUL-2001 (first entry)
XX DE Reactive oxygen species inhibitory peptide #6.
XX KW ROS; reactive oxygen species; metal binding; ischemia;
XX KW neurodegenerative.
XX OS Synthetic.
XX PN WO200125265-A1.
XX PD 12-APR-2001.
XX PF 29-SEP-2000; 2000WO-US26952.
XX PR 01-OCT-1999; 99US-0157404.
XX PR 13-JUN-2000; 2000US-0211078.

XX PA (BARO/) BAR-OR D.
XX PA (CURT/) CURTIS C G.
XX PA (LAUE/) LAU E.
XX PA (RAON/) RAO N K R.
XX PA (WINK/) WINKLER J V.
XX PA (CROO/) CROOK W M.
XX PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
XX WPI; 2001-328322/34.
XX PT Metal binding peptide compounds prevent damage by reactive oxygen
XX PT species in animal organs and tissues, useful for reperfusion,
XX PT transplantation and treating e.g. ischemia, neurological and
XX PT cardiovascular diseases -
XX PS Example 10; Page 43; 124pp; English.
XX CC The present invention relates to metal binding peptides that prevent
XX CC damage by reactive oxygen. The peptides may be used for reperfusion,
XX CC an ischemic tissue or organ with cerebral or cardiovascular ischemia,
XX CC for treating neurological trauma and for neurodegenerative disease.
XX CC The present sequence is a reactive oxygen species inhibitory peptide.

XX SQ Sequence 12 AA;
Query Match 100.0%; Score 58; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
Db 2 AHKSEVAHRFK 12

RESULT 6
AAE14801

ID	AAE14801 standard; peptide; 12 AA.
AC	AAE14801;
XX	AAE14801;
XX	24-FEB-2003 (first entry)
DT	
XX	
DE	Human reactive oxygen species generation inhibiting peptide #1.
XX	
KW	Reactive oxygen species; ROS; metal-binding peptide; angiogenesis;
KW	embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;
KW	connective tissue disorder; ocular angiogenic disease; polyposis;
KW	cardiovascular disease; cerebral vascular disease; immune disorder;
KW	sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;
KW	cancer; cystic fibrosis; diabetes; hepatitis C; infertility;
KW	inflammation; inflammatory bowel disease; neurological disease;
KW	multiple sclerosis; pancreatitis; human.
XX	
OS	Homo sapiens.
XX	
PN	WO200264620-A2.
XX	
PD	22-AUG-2002.
XX	
XX	13-FEB-2002; 2002WO-US04275.
PF	
XX	13-FEB-2001; 2001US-268558P.
PR	22-MAR-2001; 2001US-0816679.
PR	04-APR-2001; 2001US-281648P.
PR	11-APR-2001; 2001US-283507P.
PR	
PA	(DMIB-) DMI BIOSCIENCES INC.
XX	
PI	Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
PI	WPI; 2002-691590/74.
XX	
DR	
XX	New method for the inhibition of angiogenesis and the treatment of
PT	angiogenic disease, sepsis, and a disease involving acidosis, comprises
PT	the administration of a specified peptide or its salt -
PT	
XX	Example 10; Page 56; 129pp; English.
PS	
XX	
CC	The invention relates to a method for reducing molecular, cellular
CC	and tissue damage done by reactive oxygen species (ROS) and also
CC	reducing concentration of a metal ion in an animal using specific
CC	metal-binding peptides and their derivatives that bind metal ions.
CC	The compounds of the invention are useful for inhibiting angiogenesis
CC	(including required for embryo implantation e.g. in endometriosis), and
CC	for treating angiogenic diseases, such as tumour (preferably a benign
CC	tumour), tumour metastasis, hypertrophy, connective tissue disorder,
CC	psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral
CC	vascular disease, polyposis, obesity, immune disorder, sepsis, and a
CC	disease or condition involving acidosis. The compounds are also useful in
CC	the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension,
CC	senility and impotence), arthritis, asthma, autoimmune diseases,
CC	cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's
CC	disease, cystic fibrosis, (neuro)degenerative diseases, diabetes
CC	(diabetic retinopathy, renal disease, impotence and peripheral vascular
CC	disease), eye diseases, emphysema, head and traumatic brain injury,
CC	hepatitis C, infertility, inflammation, inflammatory bowel disease,
CC	metastasis, ischaemia, neoplastic diseases, neurological diseases,
CC	multiple sclerosis, pancreatitis, peripheral vascular disease, prion
CC	disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock,
CC	tissue damage, toxic reactions (e.g. poisoning (herbicide, transition
CC	metal, carbon monoxide, and antibiotic toxicity). The present
CC	sequence is a human peptide that inhibits generation of reactive
CC	oxygen species (ROS).
XX	
SQ	Sequence 12 AA;
	Query Match 100.0%; Score 58; DB 23; Length 12;
	Best Local Similarity 100.0%; Pred. No. 8e-05;
	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

Query Match	100.0%;	Score 58;	DB 23;	Length 12;
Best Local Similarity	100.0%;	Pred. No. 8e-05;		
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	AHKSEVAHRFK 11
Db	2	AHKSEVAHRFK 12
RESULT 7		
AAE14804		
ID	AAE14804	standard; peptide; 12 AA.
XX	AC	AAE14804;
XX	DT	24-FEB-2003 (first entry)
XX	XX	Human reactive oxygen species generation inhibiting peptide #4.
DE	XX	Reactive oxygen species; ROS; metal-binding peptide; angiogenesis;
KW	KW	embryo implantation; endometriosis; tumour; hypertrophy; psoriasis;
KW	KW	connective tissue disorder; ocular angiogenic disease; polyposis;
KW	KW	cardiovascular disease; cerebral vascular disease; immune disorder;
KW	KW	sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease;
KW	KW	cancer; cystic fibrosis; diabetes; hepatitis C; infertility;
KW	KW	inflammation; inflammatory bowel disease; neurological disease;
XX	XX	multiple sclerosis; pancreatitis; human.
OS	OS	Homo sapiens.
OS	OS	Synthetic.
XX	XX	
FT	Key	Location/Qualifiers
FT	Modified-site 1	/note= "N-terminal acetylated"
XX	XX	WO200264620-A2.
XX	XX	22-AUG-2002.
XX	XX	13-FEB-2002; 2002WO-US04275.
XX	XX	13-FEB-2001; 2001US-268558P.
PR	PR	22-MAR-2001; 2001US-0816679.
PR	PR	04-APR-2001; 2001US-281648P.
PR	PR	11-APR-2001; 2001US-283507P.
XX	XX	(DMIB-) DMI BIOSCIENCES INC.
XX	XX	Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;
PI	PI	WPI; 2002-691590/74.
XX	XX	New method for the inhibition of angiogenesis and the treatment of
PT	PT	angiogenic disease, sepsis, and a disease involving acidosis, comprises
PT	PT	the administration of a specified peptide or its salt -
XX	XX	Example 10; Page 57; 129pp; English.
XX	XX	The invention relates to a method for reducing molecular, cellular
CC	CC	and tissue damage done by reactive oxygen species (ROS) and also
CC	CC	reducing concentration of a metal ion in an animal using specific
CC	CC	metal-binding peptides and their derivatives that bind metal ions.
CC	CC	The compounds of the invention are useful for inhibiting angiogenesis
CC	CC	(including required for embryo implantation e.g. in endometriosis), and
CC	CC	for treating angiogenic diseases, such as tumour (preferably a benign
CC	CC	tumour), tumour metastasis, hypertrophy, connective tissue disorder.
CC	CC	psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral
CC	CC	vascular disease, polyposis, obesity, immune disorders, sepsis, and a
CC	CC	disease or condition involving acidosis. The compounds are also useful in
CC	CC	the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension,
CC	CC	senility and impotence), arthritis, asthma, autoimmune diseases,
CC	CC	cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's
CC	CC	disease, cystic fibrosis, (neuro)degenerative diseases, diabetes
CC	CC	(diabetic retinopathy, renal disease, impotence and peripheral vascular
CC	CC	disease), eye diseases, emphysema, head and traumatic brain injury,
CC	CC	hepatitis C, infertility, inflammation, inflammatory bowel disease,

CC arterial hypertension; peripheral vascular disease;
CC diabetic retinopathy, renal disease, impotence and peripheral vascular
CC diseases); eye diseases, emphysema, head and traumatic brain injury,
CC hepatitis C, infertility, inflammation, inflammatory bowel disease,

CC

CC metastasis, ischaemia, neoplastic diseases, neurological diseases,
 CC multiple sclerosis, pancreatitis, peripheral vascular disease, prion
 CC disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock,
 CC tissue damage, toxic reactions (e.g. poisoning (herbicide, transition
 CC metal, carbon monoxide, and antibiotic toxicity). The present
 CC sequence is a human peptide that inhibits generation of reactive
 CC oxygen species (ROS).
 XX
 XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 58; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
 |||||
 Db 2 AHKSEVAHRFK 12

RESULT 8

ABB99709
 ID ABB99709 standard; peptide; 12 AA.

XX AC ABB99709;

XX DT 28-MAR-2003 (first entry)

XX DE Biopolymer marker indicative of congestive heart failure.

XX KW Biopolymer marker; congestive heart failure.

XX OS Homo sapiens.

XX PN WO20028723-A2.

XX PD 07-NOV-2002.

XX PF 26-APR-2002; 2002WO-CA00611.

XX PR 30-APR-2001; 2001US-0846347.

XX PA (SYNX-) SYN.X PHARMA INC.

XX PI Jackowski G, Thatcher B, Vrees T, Yantha J, Marshall J;

XX DR WPI; 2003-111906/10.

XX PT New biopolymer marker for use in diagnostic assays for the detection or
 PT characterization of a particular disease state, especially congestive
 PT heart failure

XX PS Claim 1; Page 28; 28pp; English.

XX CC The present sequence represents a biopolymer marker which is indicative
 CC of congestive heart failure. The biopolymer marker is used for
 CC evidencing and categorizing a disease state. It is used in an assay
 CC diagnostic kit and in diagnosing, determining risk-assessment, and
 CC identifying therapeutic avenues related to a disease state, such as
 CC congestive heart failure. Controlling the presence or absence of the
 CC biopolymer marker is used to regulate a disease state.

SQ Sequence 12 AA;

Query Match 100.0%; Score 58; DB 24; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
 |||||
 Db 2 AHKSEVAHRFK 12

RESULT 9

AAW74538
 ID AAW74538 standard; peptide; 13 AA.

XX AC AAW74538;

XX DT 02-DEC-1998 (first entry)

XX DE Human serum albumin fragment.

XX KW Human; zonula occludens toxin receptor; ZOT receptor;

XX KW agonist; antagonist; toxin; anti-inflammatory drug; antibody;

XX KW gastrointestinal; inflammatory bowel disease; food allergy;

XX KW protein losing enteropathy; coeliac disease; adsorption enhancer;

XX KW fusion protein; serum albumin.

XX OS Homo sapiens.

XX PN WO9837096-A1.

XX PD 27-AUG-1998.

XX PF 18-FEB-1998; 98WO-US02257.

XX PR 17-FEB-1998; 98US-0024198.

XX PR 20-FEB-1997; 97US-0803364.

XX PA (UYMA-) UNIV MARYLAND BALTIMORE.

XX PI Fasano A;

XX DR WPI; 1998-467493/40.

XX PT New zonula occludens toxin receptors - for identifying receptor
 PT antagonists which can be used as anti-inflammatory drugs and
 PT agonists useful as intestinal/nasal adsorption enhancers

XX PS Example 7; Page 49; 68pp; English.

XX CC This is the amino acid sequence of a fragment of the human serum
 CC albumin used in the method of the invention where human zonula
 CC occludens toxin (ZOT) receptor is used. The ZOT receptor is used
 CC as capture ligand in affinity assays for agonists and antagonists
 CC of the toxin. Antagonists of ZOT are specifically useful as
 CC anti-inflammatory drugs in the treatment of gastrointestinal
 CC conditions that display an increased intestinal permeability, e.g.
 CC inflammatory bowel diseases, protein losing enteropathy, food
 CC allergies, and coeliac disease. Agonists of ZOT can rapidly open
 CC tight junctions in a reversible and reproducible manner and are
 CC useful as intestinal or nasal adsorption enhancers. The receptors
 CC are also useful for generating monoclonal or polyclonal antibodies
 CC (using conventional techniques), and to purify ZOT and fusion
 CC proteins comprising ZOT by affinity chromatography.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 58; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.7e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHKSEVAHRFK 11
 |||||
 Db 1 AHKSEVAHRFK 11

RESULT 10

ABG75657

ID ABG75657 standard; Peptide; 13 AA.

XX AC ABG75657;

XX DT 13-MAY-2003 (first entry)

XX DE Congestive heart failure disease specific marker #2.

```

XX Biopolymer marker; serum albumin; disease specific marker;
KW congestive heart failure.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Residue is optionally absent"
FT Misc-difference 13 /note= "Residue is optionally absent"
FT
XX
XX US2002160417-A1.
XX
XX 31-OCT-2002.
XX
XX 30-APR-2001; 2001US-0845726.
XX
XX 30-APR-2001; 2001US-0845726.
XX
XX (JACK/) JACKOWSKI G.
XX (STAN/) STANTON E B.
XX (THAT/) THATCHER B.
XX (VREE/) VREERES T.
XX (YANT/) YANTHA J.
XX (MAR/) MARSHALL J.
XX
XX Jackowski G, Stanton EB, Thatcher B, Vrees T, Yantha J;
XX Marshall J;
XX
XX WPI; 2003-246641/25.
XX
XX Novel biopolymer marker such as serum albumin having specific molecular
XX weight, useful in indicating disease state such as congestive heart
XX failure -
XX
XX Disclosure; Fig 1; 10pp; English.
XX
XX The invention relates to a biopolymer marker such as serum albumin having
XX a molecular weight of about 1424 daltons, useful in indicating at least
XX one particular disease state. The biopolymer marker is useful for
XX indicating at least one particular disease state such as congestive heart
XX failure and as an antigen in immunoassays for the detection of those
XX individuals suffering from the disease known to be evidenced by the
XX marker sequence. The biopolymer marker rapidly and accurately diagnoses a
XX disease state such as congestive heart failure and allows physicians to
XX identify asymptomatic patients before they develop the disease state.
XX This sequence represents a congestive heart failure disease specific
XX marker.
XX
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 58; DB 24; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 8.7e-05;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AHKSEVAHRFK 11
XX | | | | | | | | | |
XX Db 2 AHKSEVAHRFK 12
XX
XX RESULT 11
XX AAB12462
XX ID AAB12462 standard; Peptide; 20 AA.
XX
XX AC AAB12462;
XX
XX 25-OCT-2000 (first entry)
XX
XX Human albumin epitope peptide #1.
XX
XX Monoclonal antibody; hybridoma cell; immunoglobulin; IgG; fusion;
XX human albumin; diabetic nephropathy; diagnosis.

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XX Homo sapiens.
XX
XX JP2000139460-A.
XX
XX 23-MAY-2000.
XX
XX 02-NOV-1998; 98JP-0311677.
XX
XX 02-NOV-1998; 98JP-0311677.
XX
XX (TOYW ) TOYOTA CHUO KENKYUSHO KK.
XX (AISE ) AISIN SEIKI KK.
XX
XX WPI; 2000-433935/38.
XX
XX Hybridoma cells for preparation of IgG monoclonal antibody capable of
XX rapid reaction with human albumin for diagnosis of diabetic nephropathy
XX
XX Example; Fig 1; 11pp; Japanese.
XX
XX The present invention describes hybridoma cells used for preparing an
XX immunoglobulin G (IgG) monoclonal antibody capable of rapid reaction
XX with human albumin. The hybridoma cells are prepared by fusion of mamal
XX myeloma cells and spleen cells immunised with human serum albumin, and
XX producing IgG monoclonal antibody which rapidly react with human
XX albumin. The monoclonal antibodies can be used in the diagnosis of
XX diabetic nephropathy. The present sequence represents a human albumin
XX epitope peptide sequence which is used in an example from the present
XX invention.
XX
XX Sequence 20 AA;
XX
XX Query Match 100.0%; Score 58; DB 21; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 0.00014;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AHKSEVAHRFK 11
XX | | | | | | | | | |
XX Db 3 AHKSEVAHRFK 13
XX
XX RESULT 12
XX ABG75942
XX ID ABG75942 standard; peptide; 26 AA.
XX
XX AC ABG75942;
XX
XX 08-MAY-2003 (first entry)
XX
XX Human serum albumin biopolymer marker peptide.
XX
XX Human; serum albumin; biopolymer marker; SELDI;
XX Surface Enhanced Laser Desorption Ionization mass spectrometry;
XX time-of-flight detection procedure; complement system disease;
XX syndrome X; insulin resistance; hyperinsulinaemia.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 1 /note= "Optionally absent"
XX
XX Misc-difference 2..25 /note= "Specifically claimed in claim 1"
XX
XX Misc-difference 26 /note= "Optionally absent"
XX
XX US2002160531-A1.
XX
XX 31-OCT-2002.
XX
XX 30-APR-2001; 2001US-0846328.

```


XX PR 30-APR-2001; 2001US-0846328.
XX PA (JACK/) JACKOWSKI G.
XX PA (THAT/) THATCHER B.
XX PA (MARS/) MARSHALL J.
XX PA (YANT/) YANTHA J.
XX PA (VREE/) VREES T.
XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX WPI; 2003-246645/25.
XX A new biopolymer marker useful in indicating a particular disease state
XX particularly insulin resistance -
XX Disclosure; Fig 1; 10pp; English.
XX The invention describes a biopolymer marker useful in indicating at
XX least one particular disease state. Biopolymer markers are identified
XX using Surface Enhanced Laser Desorption Ionization (SELDI) mass
XX spectrometry and time-of-flight detection procedures. The markers are
XX useful for indicating e.g. complement system diseases and syndrome X,
XX characterised by the clustering of insulin resistance and
XX hyperinsulinaemia. This is the amino acid sequence of a human serum
XX albumin biopolymer marker useful for indicating insulin resistance.
XX SQ Sequence 26 AA;
Query Match 100.0%; Score 58; DB 24; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AHKSEVAHRFK 11
Db 3 AHKSEVAHRFK 13
RESULT 13
ABU09223
ID ABU09223 standard; peptide; 28 AA.
XX AC ABU09223;
XX DT 13-JUN-2003 (first entry).
XX DE Serum albumin insulin resistance disease specific marker.
XX KW Human; insulin resistance; serum albumin; biopolymer marker; lipaemia;
XX KW complement system disease; syndrome X; obesity; hyperinsulinaemia;
XX KW glucose intolerance; blood coagulation abnormality; hyperuricaemia;
XX KW albuminuria; kidney failure; stroke; hypertension; diabetes;
XX KW heart failure.
XX OS Homo sapiens.
XX PF 30-APR-2001; 2001US-0846329.
XX FH Key Location/Qualifiers
XX FT Region 2..27
XX FT /note= "Specifically claimed in claim 1"
XX PN US2002161177-A1.
XX PD 31-OCT-2002.
XX PF 30-APR-2001; 2001US-0846329.
XX PR 30-APR-2001; 2001US-0846329.
XX PA (JACK/) JACKOWSKI G.
XX PA (THAT/) THATCHER B.
XX PA (MARS/) MARSHALL J.
XX PA (YANT/) YANTHA J.
XX PA (VREE/) VREES T.

XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX WPI; 2003-361743/34.
XX DR Serum albumin biopolymer marker having specific molecular weight
XX PT indicates at least one particular disease state -
XX Disclosure; Fig 1; 10pp; English.
XX The invention relates to a serum albumin biopolymer marker having a
XX molecular weight of 2937 daltons which indicates at least one particular
XX disease state. The biopolymer marker is useful for indicating at least
XX one particular disease state, e.g. insulin resistance. Also for diseases
XX associated with the complement system and syndrome X such as Obesity,
XX hyperinsulinaemia, lipaemia, glucose intolerance, blood coagulation
XX abnormalities, hyperuricaemia, albuminuria, kidney failure, stroke,
XX hypertension, diabetes and heart failure. The biopolymer marker enables a
XX diagnostician to gain the ability to characterise either the presence or
XX absence of the disease state relative to recognition of the presence
XX and/or the absence of the biopolymer. The present sequence represents the
XX amino acid sequence of the serum albumin insulin resistance disease
XX specific marker.
XX SQ Sequence 28 AA;
Query Match 100.0%; Score 58; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AHKSEVAHRFK 11
Db 3 AHKSEVAHRFK 13
RESULT 14
AAO11631
ID AAO11631 standard; Protein; 113 AA.
XX AC AAO11631;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 25523.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US04927.
XX PR 28-FEB-2000; 2000US-0515126.
XX PR 18-MAY-2000; 2000US-0577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX DR N-PSDB; AAI91562.
XX PT Isolated nucleic acids and polypeptides, useful for preventing
XX diagnosing and treating e.g. leukaemia, inflammation and immune
XX disorders -
XX PS Claim 20; SEQ ID NO 25523; 1399pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 113 AA;
 Query Match 100.0%; Score 58; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
 Db 30 AHKSEVAHREFK 40
 |||||

RESULT 15
 AAO02642
 ID AAO02642 standard; Protein: 116 AA.
 XX AC AAO02642;
 DT 06-NOV-2001 (first entry)
 DE Human polypeptide SEQ ID NO 16534.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX OS Homo sapiens.

XX PN WO200164835-A2.
 XX PD 07-SEP-2001.
 XX PF 26-FEB-2001; 2001WO-US04927.
 XX PR 28-FEB-2000; 2000US-0515126.
 XX PR 18-MAY-2000; 2000US-0577409.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX DR WPI; 2001-514838/56.
 XX DR N-PSDB; AAI82573.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX PS Claim 20; SEQ ID NO 16534; 1399pp + Sequence Listing; English.
 XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 116 AA;
 Query Match 100.0%; Score 58; DB 22; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AHKSEVAHREFK 11
 Db 23 AHKSEVAHREFK 33
 |||||

Search completed: August 29, 2003, 14:26:28
 Job time : 84 secs